

Figure 1A

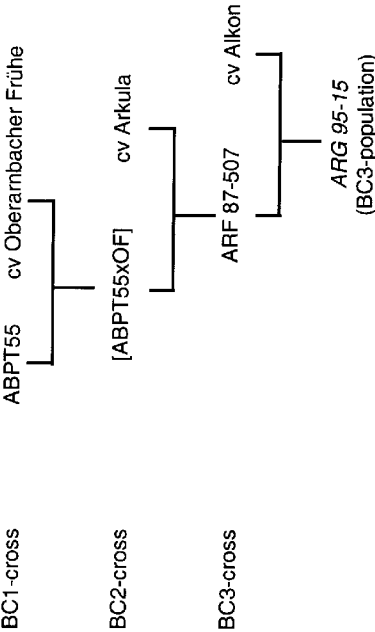


Figure 1B

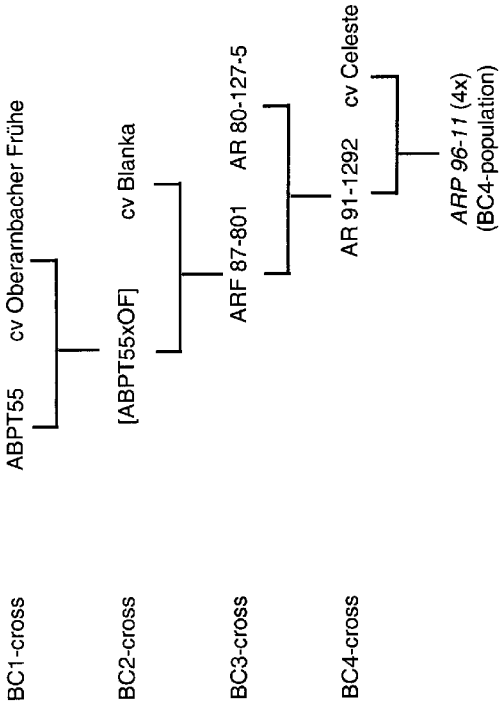


Figure 1C

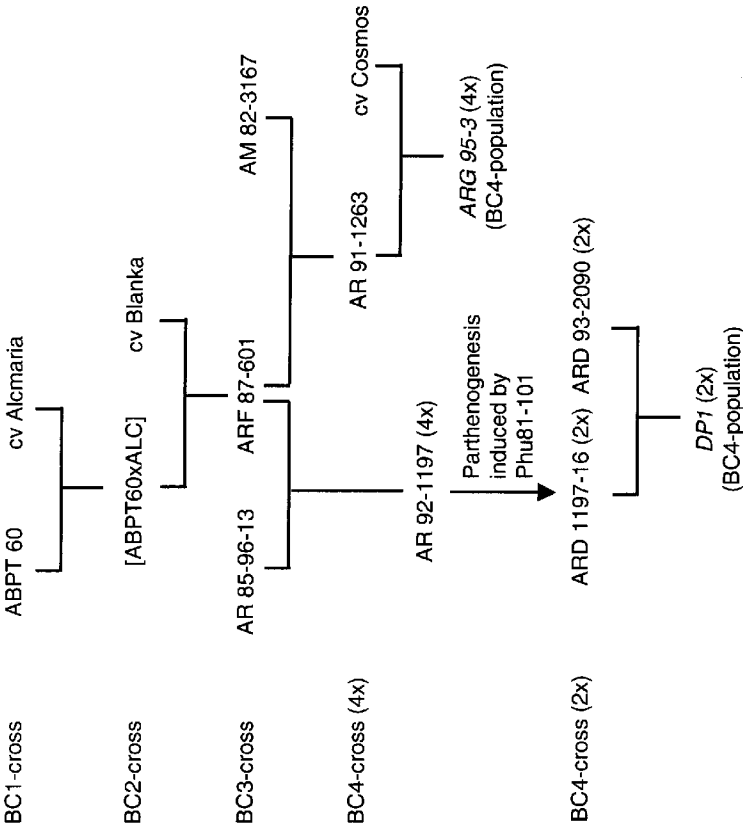
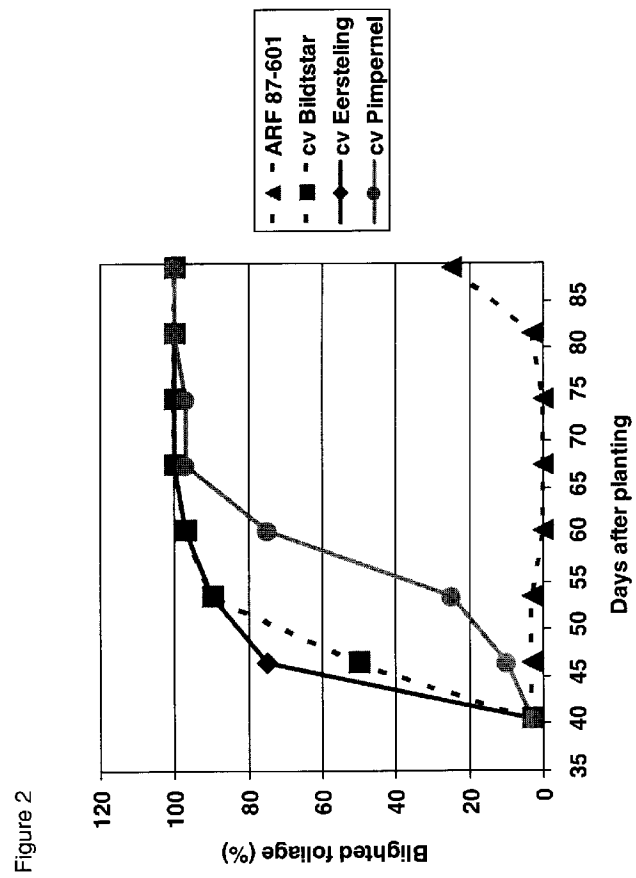


Figure 1D

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Figure 3

* ARF 87-507 and ARF 87-601 had identical disease progress curves

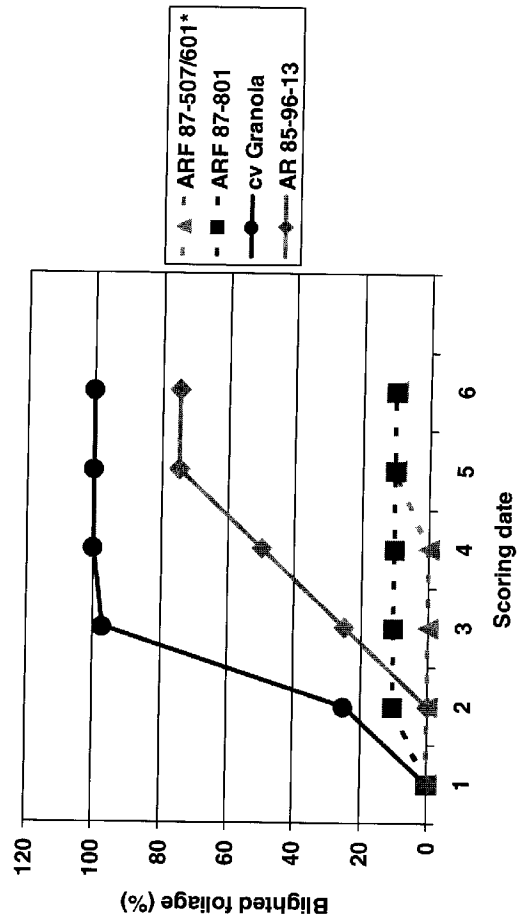




Figure 4



Figure 4 dia 3



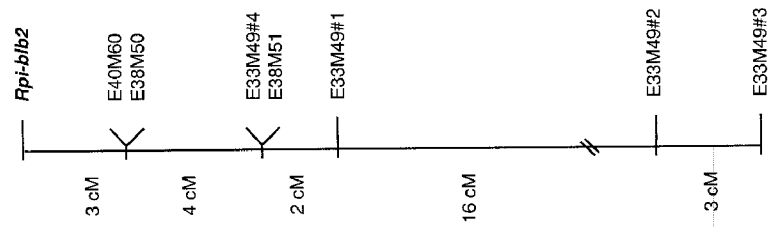
Figure 4 dia 4



Figure 4 dia 5

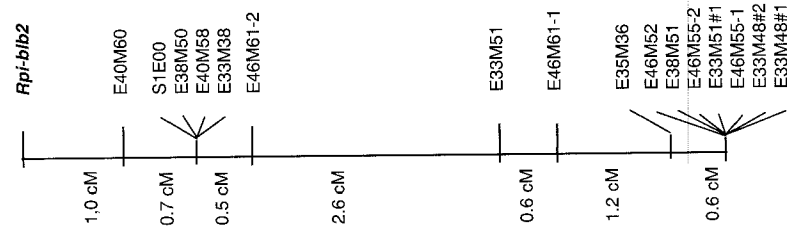


Figure 4 dia 6



ARG 95-15

Figure 5



ARG 95-3

Figure 6

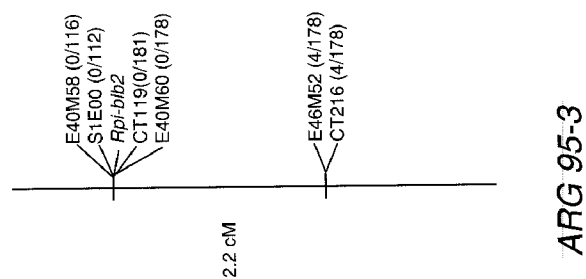


Figure 7

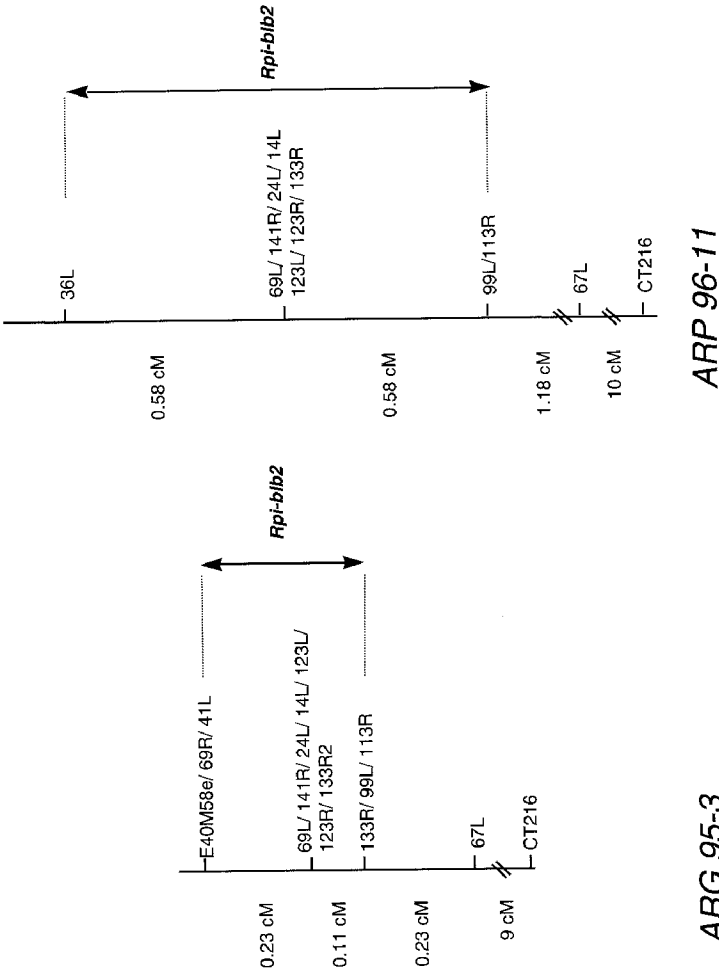
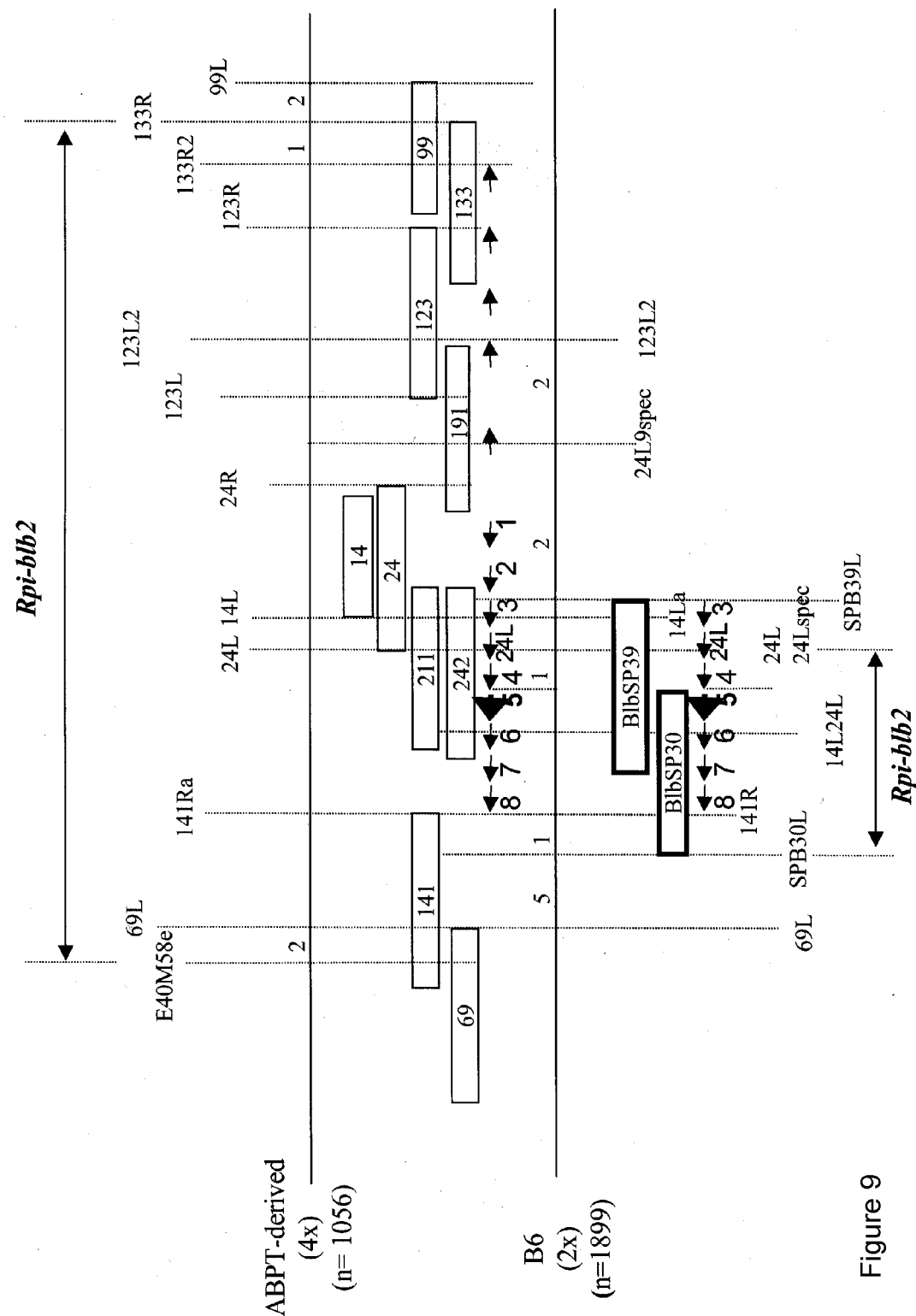


Figure 8



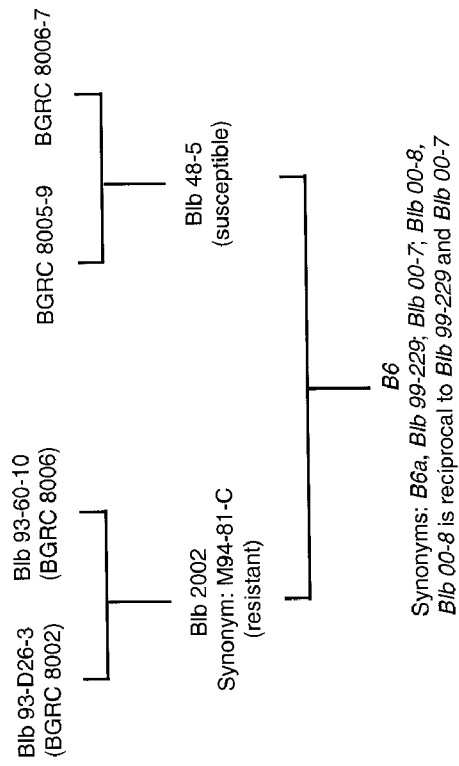


Figure 10

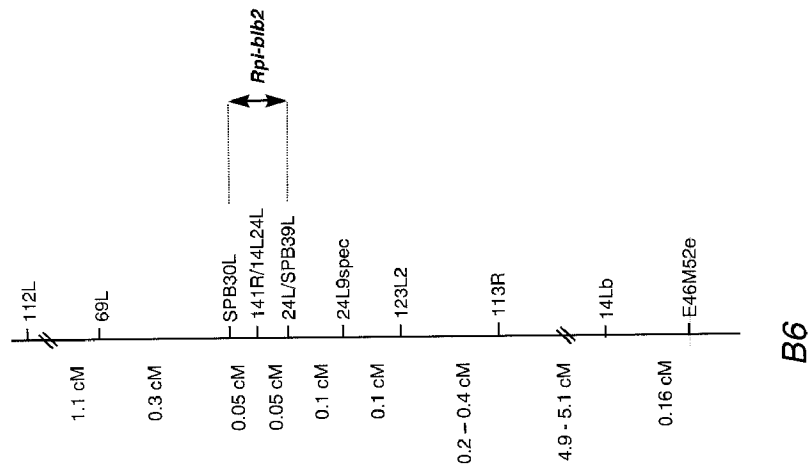


Figure 11

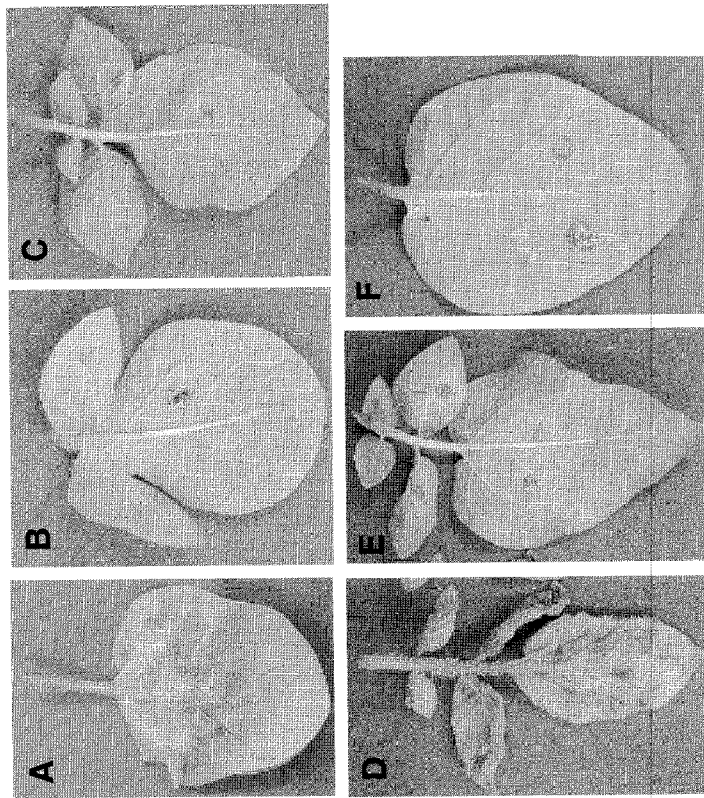


Figure 12

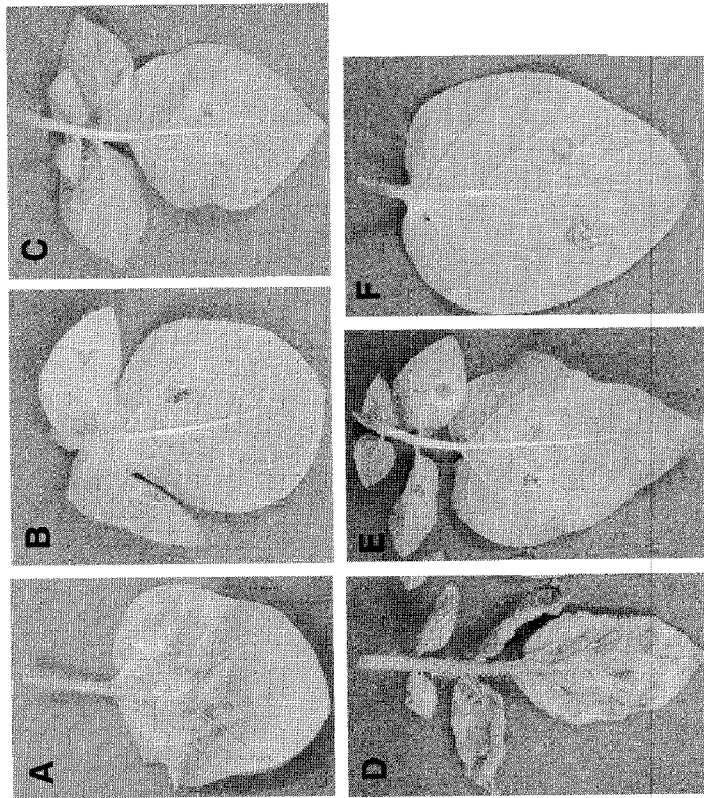


Figure 12 dia2

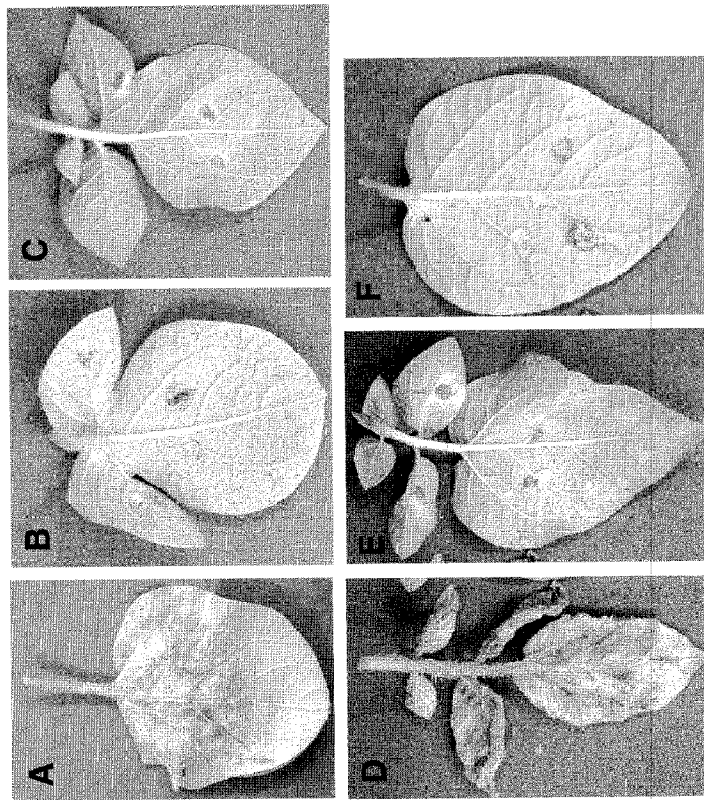


Figure 12 dia 3

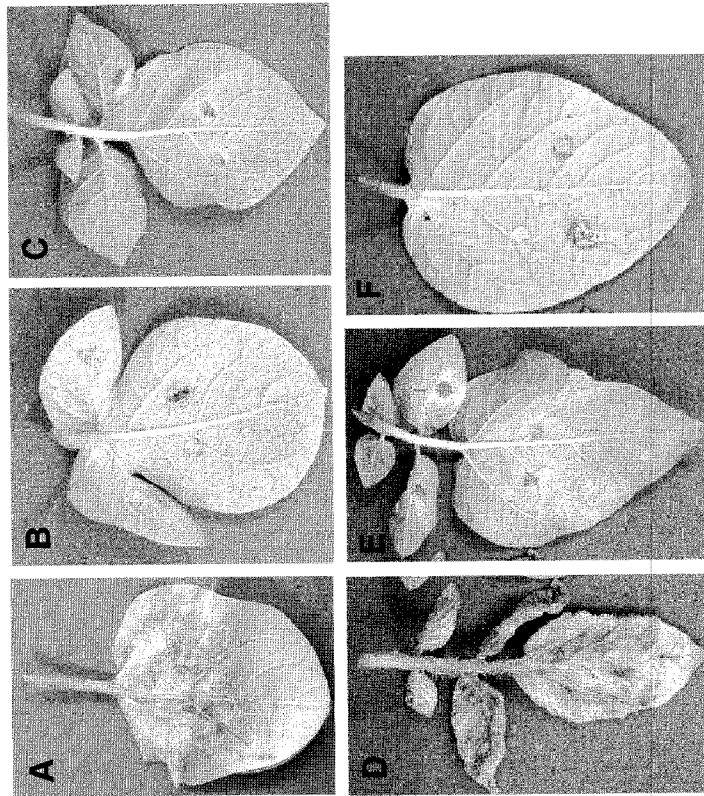


Figure 12 dia 4

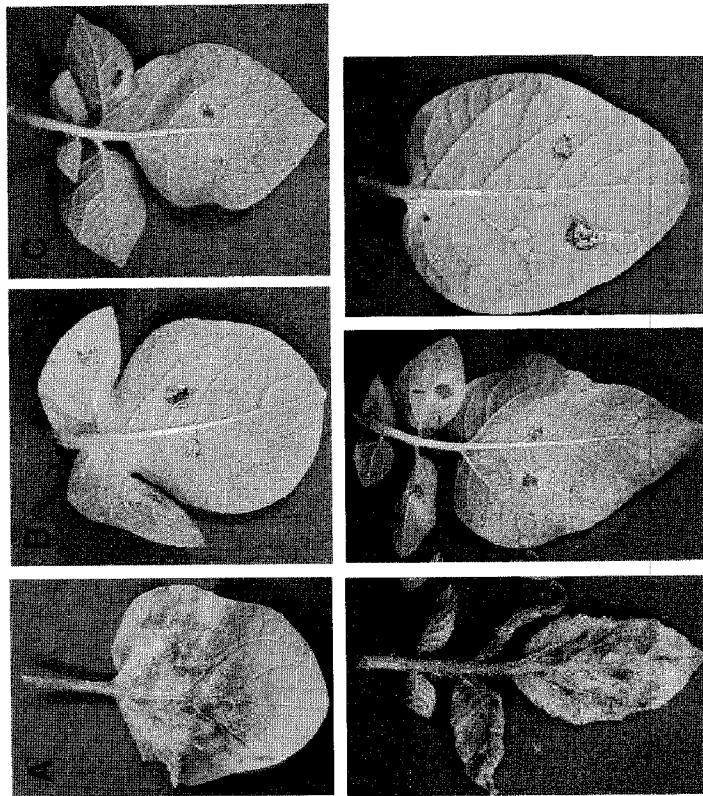


Figure 12 dia 5

Figure 13A

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TAAAGAATGAAGAAGATCAAAGGCTGTTGATGTGGATCTGATTGAAAGC 150
CTGAAATTGAAGCTGACATTTATTTGTACATATGTCCAGCTTTCTTATTC 200
CGATTTGGAGAAGTTTGAAGATATAATGACTAGAAAAAGACAAGAGGTTG 250
AGAATCTGCTTCAACCAATTTTGGATGATGATGGCAAAGACGTCGGGTGT 300
AAATATGTCCTTACTAGCCTCGCCGGTAATATGGATGACTGTATAAGCTT 350
GTATCATCGTTCTAAATCAGATGCCACCATGATGGATGAGCAATTGGGCT 400
TCCTCCTCTTGAATCTCTCTCATCTATCCAAGCATCGTGCTGAAAAGATG 450
TTTCCTGGAGTGACTCAATATGAGGTTCTTCAGAATGTATGTGGCAACAT 500
AAGAGATTTCCATGGATTGATAGTGAATTGTTGCATTAAGCATGAGATGG 550
TTGAGAATGTCTTATCTCTGTTTCAACTGATGGCTGAGAGAGTAGGACGC 600
TTCCTTTGGGAGGATCAGGCTGATGAAGACTCTCAACTCTCCGAGCTAGA 650
TGAGGATGATCAGAATGATAAAGACCCTCAACTCTTCAAGCTAGCACATC 700
TACTCTTGAAGATTGTTCCAACCTGAATTGGAGGTTATGCACATATGTTAT 750
AAAACCTTTGAAAGCTTCAACTTCAACAGAAATTGGACGCTTCATTAAGAA 800
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AAGAGCATATGATAACTGTTATTACCCCTAACACTTCAGGGGCTCGAAAC 900
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TAGCACTTACCAGGGAGGTATCAACTCTTGACGCGACTTGGAAGAGAAA 1050
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TCTGGAATAATTGAACTCCTTAAGGAAGATCTCAAACATGTTTATCTGA 1150
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TTCATGCATCTGCTACAGAGACACTTAGATGATTTGCTGGATTCCAATGC 1250
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AGATTCAATTATTGTTTCGAGATAATGGTCTCTTACATCTTATTTCTCAC 1450
TTCCCATTACCAGAAAGAAGATGATGCTTATCAAAGAAGAGGTCTCTGAT 1500
TTACATGAGAACATTTCCAAGAACAGAGGTCTCATCGTTGTGAACCTCTCC 1550
CAAGAAACCAGTTGAGAGCAAGTCATTGACAACCTGATAAAATAATTGTAG 1600
GTTTTGGTGAGGAGACAACTTGATACTTAGAAAGCTCACCAAGTGGACCG 1650
```


Figure 13A (cont.)

GCAGATCTAGATGTCATTTTCGATCATTTGGTATGCCGGGTTTAGGTAAAAC 1700
TACTTTGGCGTACAAAGTATACAATGATAAATCAGTTTCTAGCCATTTTCG 1750
ACCTTCGTGCATGGTGCACGGTCGACCAAGTATATGACGAGAAGAAGTTG 1800
TTGGATAAAATTTTCAATCAAGTTAGTGACTCAAATTCAAAATTGAGTGA 1850
GAATATTGATGTTGCTGATAAACTACGGAAACAATTGTTTGAAAGAGGT 1900
ATCTTATTGTCTTAGATGACGTGTGGGATACTAATACATGGGATGAGCTA 1950
ACAAGACCTTTTCCTGATGGTATGAAAGGAAGTAGAATTATTTTGACAAC 2000
TCGAGAAAAGAAAGTTGCTTTGCATGGAAAGCTCTACACTGATCCTCTTA 2050
ACCTTCGATTGCTAAGATCAGAAGAAAGTTGGGAGTTATTAGAGAAAAGG 2100
GCATTTGGAAACGAGAGTTGCCCTGATGAACTATTGGATGTTGGTAAAGA 2150
AATAGCCGAAAATTGTAAAGGGCTTCCTTTGGTGGTGGATCTGATTGCTG 2200
GAATCATTGCTGGGAGGGAAAAGAAAAGAGTGTGTGGCTTGAAGTTGTA 2250
AATAATTTGCATTCCCTTATTTTGAAGAATGAAGTGGAAGTGATGAAAGT 2300
TATAGAAATAAGTTATGACCACTTACCTGATCACCTGAAGCCATGCTTGC 2350
TGTACTTTGCAAGTGCGCCGAAGGACTGGGTAACGACAATCCATGAGTTG 2400
AAACTTATTTGGGGTTTTGAAGGATTTGTGGAAAAGACAGATATGAAGAG 2450
TCTGGAAGAAGTGGTGAAAATTTATTTGGATGATTTAATTTCCAGTAGCT 2500
TG GTAATTTGTTTCAATGAGATAGGTGATTACCTACTTGCCAACTTCAT 2550
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GCATTGATTATGATGATGATGAAGAGCACTTTGGGCTTAATTTTGTCTG 2700
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GACACTTGAGGCTTCTTAGAACCTTGACCTGGAATCCTCTTTTATCATG 2850
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TCTGGAATCTAGAAATCTTGTGTTGTGGATAACAAAGAATCAACCTTGATA 3000
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TGCTTGTTCTTTCTTTGATATGGATGCAGATGAATCAATACTGATAGCAG 3100
AGGACACAAAGTTAGAGAACTTGACAGCATTAGGGGAACTCGTGCTTTCC 3150
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GCTTCATTTCAACTCAAGGAGTCATGGGATTATTCAACAGAGCAATATT 3250
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TTTGAAAGATCAAACACAAATGACAGTGGGTCTCTGCAGCCATAAATCG 3350
GCCATGGGATTTTCACTTTCCTTCGAGTTTGAAAAGATTGCAATTGCATG 3400

Figure 13A (cont.)

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CATGGGAGAAGAAGACACCTTTGAGAATCTCAAATGTTTGATGTTGAGTC 3550
AAGTGATTCTTTCCAAGTGGGAGGTTGGAGAGGAATCTTTTCCCACGCTT 3600
GAGAAATTAGAACTGTCGGACTGTCATAATCTTGAGGAGATTCCGTCTAG 3650
TTTTGGGGATATTTATTCCTTGAAAATTATCGAACTTGTAAGGAGCCCTC 3700
AACTTGAAAATTCGCTCTCAAGATTAAGGAATATGCTGAAGATATGAGG 3750
GGAGGGGACGAGCTTCAGATCCTTGGCCAGAAGGATATCCCGTTATTTAA 3800
GTAG 3804
```

Figure 13B

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TTTGATAGAGTGAACGTAAAGTATTGAATTGTAGATATCATGTGGCTTT 100
AAAAATTTGATATGTGTTATTTTGGCAGGAGTCATTTTCTGCTCTTCGCA 150
AGGATGCTGCCAATGTTCTGGATTTCCTAGAGAGATTAAAGAATGAAGAA 2001
GATCAAAAGGCTGTTGATGTGGATCTGATTGAAAGCCTGAAATTGAAGCT 2501
GACATTTATTTGTACATATGTCCAGCTTTCTTATTCGATTGGAGAAAGT 3001
TTGAAGATATAATGACTAGAAAAAGACAAGAGGTTGAGAATCTGCTTCAA 3501
CCAATTTTGGATGATGATGGCAAAGACGTCGGGTGTAAATATGTCCTTAC 4001
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AATCAGATGCCACCATGATGGATGAGCAATTGGGCTTCTCCTCTTGAAT 5001
CTCTCTCATCTATCCAAGCATCGTGCTGAAAAGATGTTTCTGGAGTGAC 5501
TCAATATGAGGTTCTTCAGAATGTATGTGGCAACATAAGAGATTTCCATG 6001
GATTGATAGTGAATTGTTGCATTAAGCATGAGATGGTTGAGAATGTCTTA 6501
TCTCTGTTTCAACTGATGGCTGAGAGAGTAGGACGCTTCCTTTGGGAGGA 7001
TCAGGCTGATGAAGACTCTCAACTCTCCGAGCTAGATGAGGATGATCAGA 7501
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GTTCCAACGAATTGGAGGTTATGCACATATGTTATAAAACTTTGAAAGC 8501
TTCAACTTCAACAGAAATTGGACGCTTCATTAAGAAGCTCCTGGAAACCT 9010
CTCCGGACATTCTCAGAGAATATCTGATTCATCTACAAGAGCATATGATA 9510
ACTGTTATTACCCCTAACACTTCAGGGGCTCGAAACATTCATGTCATGAT 1000
GGAATTCCTATTGATTATTCTTTCTGATATGCCGCCCAAGGACTTTATTC 1050
ATCATGACAACTTTTTGATCTCTTGGCTCGTGTTGTAGCACTTACCAGG 1100
GAGGTATCAACTCTTGTACGCGACTTGGAAGAGAAATTAAGGATTAAGA 1150
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TCTCAATATTGCTTCCCATGAGTGATGGACCTCTCTTCATGCATCTGCT 1300
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TGATAAAGGAACAAATTGGGCTGGTGAAAGAAGACTTGGAATTCATAAGA 1400
TCTTTTTTCGCGAATATGAGCAAGGATTGTATAAAGATCTCTGGGAACG 1450
TGTTCTAGATGTGGCATATGAGGCAAAAGATGTCATAGATTCAATTATTG 1500
TTCGAGATAATGGTCTCTTACATCTTATTTCTCACTTCCCATTACCAGA 1550
AAGAAGATGATGCTTATCAAAGAAGAGGTCTCTGATTTACATGAGAACAT 1600
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Figure 13B (cont.)

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ACAAACTTGATACTTAGAAAGCTCACCAGTGGACCGGCAGATCTAGATGT 1750
CATTTTCGATCATTGGTATGCCGGTTTAGGTAAAAC TACTTTGGCGTACA 1800
AAGTATACAATGATAAATCAGTTTCTAGCCATTTCGACCTTCGTGCATGG 1850
TGCACGGTCGACCAAGTATATGACGAGAAGAAGTTGTTGGATAAAATTTT 1900
CAATCAAGTTAGTGACTCAAATTCAAAATTGAGTGAGAATATTGATGTTG 1950
CTGATAAACTACGGAAACAATTGTTTGAAAGAGGTATCTTATTGTCTTA 2000
GATGACGTGTGGGATACTAATACATGGGATGAGCTAACAAGACCTTTTCC 2050
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TTGCTTTGTCATGGAAAGCTCTACACTGATCCTCTTAACCTTCGATTGCTA 2150
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GAGTTGCCCTGATGAAC TATTGGATGTTGGTAAGAAATAGCCGAAAATT 2250
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CTTTATTTTGAAGAATGAAGTGGAAGTGATGAAAGTTATAGAAATAAGTT 2400
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GCGCCGAAGGACTGGGTAACGACAATCCATGAGTTGAAACTTATTTGGGG 2500
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TGAAAATTTATTTGGATGATTTAATTTCCAGTAGCTTGGTAATTTGTTTC 2600
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CAAGTGCTCCATCAGATTTGTTGCCACGTCAAATTAGCATTGATTATGAT 2750
GATGATGAAGAGCACTTTGGGCCTTAATTTTGTCTGTTCGGTTCAAATAA 2800
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CAGAAGTTAAATCTCTGCCTTTGTCTTTCTCAAACCTCTGGAATCTAGAA 3050
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AGAGGATATTTTCAAAGGCTTCCCAATCTTCAAGTGCTTCATTTCAAAC 3300
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GATTCCTAACTGAACTAGAAAACTCACTGTAGATTTTGAAAGATCAAA 3400

Figure 13B (cont.)

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ACTTTCCTTCGAGTTTGAAAAGATTGCAATTGCATGAATTCCTCTGACA 3500
TCCGATTCACCTATCAACAATAGCGAGACTGCTGAACCTTGAAGAGTTGTA 3550
CCTTTATCGTACAATCATCCATGGGGAAGAATGGAACATGGGAGAAGAAG 3600
ACACCTTTGAGAATCTCAAATGTTTGATGTTGAGTCAAGTGATTCTTTCC 3650
AAGTGGGAGGTTGGAGAGGAATCTTTCCACGCTTGAGAAATTAGAACT 3700
GTCGGACTGTCATAATCTTGAGGAGATTCCGTCTAGTTTGGGGATATTT 3750
ATTCCTTGAAAATTATCGAACTTGTAAGGAGCCCTCAACTTGAAAATTCC 3800
GCTCTCAAGATTAAGGAATATGCTGAAGATATGAGGGGAGGGGACGAGCT 3850
TCAGATCCTTGCCAGAAGGATATCCCGTTATTTAAGTAG 3890
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Figure 13C

GATCTAGAATCACCGAACCTCCCCTCGGTACAGCTCCTCCAGTTCTACCA 50
TGAATTTTCATCCACTGATTCTCTTCAATCGCCATTGCAGATTCTCTCGA 100
TCTATGCTCAAAAAATCCCGAGATAAAACCCCTAGATCTGCTTCAAATGCT 150
CTGATACCATGTAATTTTCAGTGAATTTCTAACTAAACAATGGAGAGAATTA 200
ACTATTTTAGAAAGACTGATTGAAGGAGAAGAAGAGAGAAAAATTTCTATA 250
TTGAACTCATGAACCAAATGAATGAAAAAATAATGAGAAGAACTATAC 300
TATTACAATCTATATATCTCTATTTATATTCTAATCTGAAGCAGTTAATT 350
TAACTGACTCTAACAAC TAGACTGATAGGTGTACATTTTCTGTTAGTGCA 400
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CATTTCGAATAGCTTCAATGAGAAGCAAACATGTGTACCTGTAAAGACACA 500
CAGTAAAAGTGTTAATAATGAATAAATATGAATAAATCAAATAATAAATT 550
AAAAATAAAAAACACATCCAATTAACATTGGAGGTCTTGAAAATCGATGGT 600
AATTAACAAGACCCCTTGTGAAATTTAAGTCTGTAATTGAAAATTTGAGT 650
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AATTTGTGGCAGACAAGTGAGGAGGCCCCACTGTAATTGATTCATGCTTT 750
TGCTTTCTTGACTTTTTTGAACAATACTATGCATCATATTTGGTCTTAAT 800
TATTCCCTCTGTTTATTTCCAGAATTTTGAGCTCTATACATCTAATAACAA 850
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ATACTTTCACCTCATTAATTTATTACTTACCCATGATAAGTTGTATTAAT 1150
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AGAGATAGAAAGGTTCCGTACCAGTTGGTCTCGTTTCTGGATGAACCCCA 1350
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CTTCCACTAATTAAGTCCTCTTAAGTTCGCGTGAAAATAGTGAAATTATT 1450
GATTATTCTTATCATTTTCATCTTCTTCTCCTGATAAAGTTTTATGTACT 1500
TTTTATGCATCAGGTCTTGAGAAC TTGGAAGGAAAAGTAGAATCATGGA 1550
AAAACGAAAAGATAATGAAGAAGCAACAACCTCATTTGGTATGTTATTTGA 1600
TAGAGTGAAC TGTAAGTATTGAATTGTAGATATCATGTGGCTTTAAAAA 1650

Figure 13C (cont.)

TTTGATATGTGTTATTTTGGCAGGAGTCATTTTCTGCTCTTCGCAAGGAT 17001
GCTGCCAATGTTCTGGATTTCTTAGAGAGATTAAAGAATGAAGAAGATCA 1750
AAAGGCTGTTGATGTGGATCTGATTGAAAGCCTGAAATTGAAGCTGACAT 1800
TTATTTGTACATATGTCCAGCTTTCTTATTCCGATTTGGAGAAGTTTGAA 1850
GATATAATGACTAGAAAAAGACAAGAGGTTGAGAATCTGCTTCAACCAAT 1900
TTTGGATGATGATGGCAAAGACGTCGGGTGTAAATATGTCTTACTAGCC 1950
TCGCCGGTAATATGGATGACTGTATAAGCTTGTATCATCGTTCTAAATCA 2000
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GTTTCAACTGATGGCTGAGAGAGTAGGACGCTTCTTTGGGAGGATCAGG 2250
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AACTGAATTGGAGGTTATGCACATATGTTATAAACTTTGAAAGCTTCAA 2400
CTTCAACGAAATTGGACGCTTCATTAAGAAGCTCCTGGAAACCTCTCCG 2450
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CGATCATTGGTATGCCGGGTTTAGGTAAACTACTTTGGCGTACAAAGTA 3350
TACAATGATAAATCAGTTTCTAGCCATTTGACCTTCGTGCATGGTGCAC 3400

Figure 13C (cont.)

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AAACTACGGAAACAATTGTTTGGAAAGAGGTATCTTATTGTCTTAGATGA 3550
CGTGTGGGATACTAATACATGGGATGAGCTAACAAGACCTTTTCCTGATG 3600
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TTGCATGGAAAGCTCTACACTGATCCTCTTAACCTTCGATTGCTAAGATC 3700
AGAAGAAAGTTGGGAGTTATTAGAGAAAAGGGCATTGGAACGAGAGTT 3750
GCCCTGATGAACATTTGGATGTTGGTAAAGAAATAGCCGAAAATTGTAAA 3800
GGGCTTCCTTTGGTGGTGGATCTGATTGCTGGAATCATTGCTGGGAGGGA 3850
AAAGAAAAAGAGTGTGTGGCTTGAAGTTGTAAATAATTTGCATTTCCTTA 3900
TTTTGAAGAATGAAGTGAAGTGATGAAAGTTATAGAAATAAGTTATGAC 3950
CACTTACCTGATCACCTGAAGCCATGCTTGCTGTACTTTGCAAGTGCGCC 4000
GAAGGACTGGGTAACGACAATCCATGAGTTGAACTTATTTGGGGTTTTG 4050
AAGGATTTGTGGAAGACAGATATGAAGAGTCTGGAAGAAGTGGTGAAA 4100
ATTTATTTGGATGATTTAATTTCCAGTAGCTTGGTAATTTGTTTCAATGA 4150
GATAGGTGATTACCTACTTGCCAACTTCATGATCTTGTGCATGACTTTT 4200
GTTTGATAAAAGCAAGAAAGGAAAAGTTGTGTGATCGGATAAGTTCAAGT 4250
GCTCCATCAGATTTGTTGCCACGTCAAATTAGCATTGATTATGATGATGA 4300
TGAAGAGCACTTTGGGCTTAATTTGTCTGTTTCGGTTCAAATAAGAAAA 4350
GGCATTCCGGTAAACACCTCTATTCTTTGACCATAAATGGAGATGAGCTG 4400
GACGACCATCTTTCTGATACATTTTCTAAGACACTTGAGGCTTCTTAG 4450
AACCTTGACCTGGAATCCTCTTTTATCATGGTTAAAGATTCTTTGCTGA 4500
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GTTAAATCTCTGCCTTTGTCTTTCTCAAACCTCTGGAATCTAGAAATCTT 4600
GTTTGTGGATAACAAAGAATCAACCTTGATACTATTACCGAGAATTTGGG 4650
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ATGGATGCAGATGAATCAATACTGATAGCAGAGGACACAAAGTTAGAGAA 4750
CTTGACAGCATTAGGGGAACCTGTCCTTCTTATGGAAAGATACAGAGG 4800
ATATTTTCAAAGGCTTCCCAATCTTCAAGTGCTTCATTTCAAACCTCAAG 4850
GAGTCATGGGATTATTCACAGAGCAATATTGGTTCCCGAAATTGGATTT 4900
CCTAACTGAAC TAGAAAACTCACTGTAGATTTTGAAAGATCAAACACAA 4950
ATGACAGTGGGTCTCTGCAGCCATAAATCGGCCATGGGATTTTCACTTT 5000
CCTTCGAGTTTGAAAAGATTGCAATTGCATGAATTTCTCTGACATCCGA 5050
TTCATATCAACAATAGCGAGACTGCTGAACCTTGAAGAGTTGTACCTTT 5100
ATCGTACAATCATCCATGGGGAAGAATGGAACATGGGAGAAGAAGACACC 5150

Figure 13C (cont.)

TTTGAGAATCTCAAATGTTTGATGTTGAGTCAAGTGATTCTTTCCAAGTG 5200
GGAGGTTGGAGAGGAATCTTTTCCACGCTTGAGAAATTAGAACTGTCGG 5250
ACTGTCATAATCTTGAGGAGATTCCGCTCTAGTTTTGGGGATATTTATTCC 5300
TTGAAAATTATCGAACTTGTAAGGAGCCCTCAACTTGAAAATCCGCTCT 5350
CAAGATTAAGGAATATGCTGAAGATATGAGGGGAGGGGACGAGCTTCAGA 5400
TCCTTGGCCAGAAGGATATCCCGTTATTTAAGTAGTTTTTGAGCATTATG 5450
GTTGAAAAGTAGATTGCACTTTGCTGGGTAGATTGTATATGGTTAAGAAA 5500
ATTCTGTTACAGTTGTTATGAAACATTTTTATTTGACTTTTCTGAGTTTC 5550
TTTTAGAAAACCTCAGAACTTTTTAACAAAAATTATAGTTTTTATAAATAC 5600
AATGTGGATTGTGCTTTGGCTGTCCAACCTGGTCTGAAGTCTCATATGCT 5650
CAGAGCACTATCGTTCAACCTCAATCAAGGTACTGATTTAAATGACATC 5700
TATACTACTTTATCACAAACCCAACGAACCTTTCATCTCAAAGCTAGGCC 5750
AGGAAGTGAAGAGGTTGTAGAGAGCTTATAAGCACTCATGACTTCCTTTT 5800
CTCGAACATTCAACCAACGTAGGCTGAAATCCCACTCTGAACGAAAATAA 5850
GTGTTTGTTTATCAAATTAACCTCTCGTAGTAGAACTGAAATACCTTCT 5900
TCTAAACGTTCAACAAATGGGATTTCCAGCACTCAAAGTGAATGAAAGGT 5950
TCACATTAATCTTCAAAAAGAATTACGACAATTCATGACCACAAGTACAT 6000
TGACAGCACCATTTCAACAGAAGAACAAGTCAATGCTGCATCTTCATCAA 6050
TAATCCGAGTGTCGAACCTCCTTCCTGACACTGTCCTGTATATGTAAAGT 6100
TTCTCAACAGGGCAACTTTCTGGTCTCGTATCTGGATGACCCCTCTCGTC 6150
TATAACTTCAACATTAAGCCCTGGCAACTTCTGGACCAACAGCTTACATG 6200
CTTCAAACTTACTGAACAATTAGACATCCAAAGGGATCGCATTGTCTCC 6250
AGCTTTGCAGCATTAGCCAACAGAGCCTCATCGCCAAAGGGGAGTCTCT 6300
AATCTCGAATTTGAAAAAATTGTTGTTGTATGACTTTCCTCTGACATCCG 6350
ATGCATATCAACAATAGCAAGACTGGAGGTTGGAGAGGAATCCTTTATT 6400
ATACAATCATTCAAGGAGAAGAATGGAACATGGGGGAGGAAGACACTTTT 6450
GAGAATCTGAAATGTGTTAGAGCCACAAGCTACAGAAGTATTGAATTTGT 6500
CATGAATATCAACATCTTCATCCTAGTTAATTCTTTTCAATTTTAAAT 6550
AGACTCTCATTTTAAATCACTAATATTCTTCTATTTGTGACTTCTTTTCTG 6600
CAGGTGGCAACTTTAAATTCATAAAGTATAGGATTGATGACAACTCGAA 6650
AAATATCTTAATGAGGTGAAGTTTGAGCAGTCAGCAGATGGTGGTTCCAA 6700
CTCTAAGTTGACAAGCACATACTATCCCGGAGGGCGATTTCAAGCCTGAT 6750
GCATATGGTTAGTGTGGCTAGAGCAGACAGGATGTATTACCTGGATATCT 6800
ACCAAGACGAATCCACAATCAGTTTTATGTCAAGCAATACATGAAGTAAC 6850
TCCCGATAGAACAGTAAAAGCAAGATGTGTAGGTGTATCTGACTCTAAG 6900

Figure 13C (cont.)

```
AGATTGTACATTCTCTTTGAGATTTTACTGCTAATACAAATTTACACC 6950
TCAGAAGCGAATCTAGAATTTCTAGAGCATGAATGCACCACTAATGAAAG 7000
GAGAAAAAAGGAAGTATGAAGTGGGAATTTGATCCTTGTTTCTAGGTATA 7050
TAAATTTTATCATTCAACTATACTTCATTTAGCAAACAACTCTCTTTGCC 7100
ATTATTTCTCAAACAAGGGCTTCTAATATTGCTAAACTAAAGACTGTCAA 7150
AAGGTAAGTTCATCTTCAAACCTCTCTTGTTTACTTTATCTAAAGGGGAAC 7200
TATGAAAAACAAGAAACATCAGGAATGTCCCGTAAACAAAGCAGCCTCAT 7250
GCACAAAACATCCAACGTTGGTAGGATTAATGGAGGGATCGCATCCCAGG 7300
AGGATACTGTAGAAAAATTAGTGGCTTCTTTCACCGCTCAAACCCATGAT 7350
CTATAGGTTACATGGAGACAACCTTTATGGTTGCTCGTAGGCTCCCGTCAA 7400
TTCTCATAAACCACAACACCAAAGTTGCATCAGACATCATCTTCATTCAC 7450
AAGCTGACAATCTCCACAAGTCTTAGTCAACTTGTAATATGAATATTAGC 7500
CAGGTAGACGTACATATTTACAAAATTGAGTTTCCTATATAATATGGTTT 7550
GAAGGAATGAAACATGATGGGGAGGGTAGATAAAATAATATATGAGGCAT 7600
AAAAATAGGAAAGATATTTGTAGTGAGAGGTTTTGACTTTTTATGCTGCT 7650
TTTGATCTTCAGTTTCTGTATTCTTTTTCTACTGCTTTCCTCTTCTTTC 7700
TCCTGAGTAAAGTTTTATGTAGGTACTTTTTATACGTCCGATCGTGAGAA 7750
CTTGAAAGAAAGCTCTCTATAGCTATGTTAGGTGCCACATAAAAAAATG 7800
AAATATTACAAAAACCTGATAATAAAATACACTAATCTAAGATATTCAC 7850
TGCAACATACATGCAAAATATATATATATAAATTTTCATGAAAATTATAA 7900
CAAATAATAGATGTGAACATATAACTTTAAAAATAATATTACATCCATAA 7950
AGCTTAAATTCTAGATC 7967
```

Figure 13D

GATCTGCTTCAAATGCTCTGATACCATGTAATTTTCAGTGAATTCTAACTA 50
AACAAATGGAGAGAATTAACTATTTTAGAAAGACTGATTGAAGGAGAAGAA 100
GAGAGAAAAATTCTATATTGAACTCATGAACCAAATGAATGAAAAAAT 150
AATGAGAAGAACTATACTATTACAATCTATATATCTCTATTTATATTCTA 200
ATCTGAAGCAGTTAATTTAACTGACTCTAACAAC TAGACTGATAGGTGTA 250
CATTTTCTGTTAGTGCAGTGCAGTGCATTTAACTAACTGCTTAACATAAA 300
GAATGTTGTTCTGAAC TTCATTGCAATAGCTTCAATGAGAAGCAAACATGT 350
GTACCTGTAAAGACACACAGTAAAAGTGTTAATAATGAATAAATATGAAT 400
AAATCAAATAATAAATTA AAAAATAAAAACACATCCAATTAACATTGGAGG 450
TCTTGAAAATCGATGGTAATTAACAAAGACCCTTGTGAAATTTAAGTCTG 500
TAATTGAAAATTTGAGTATAGGTTAGGGGACATTTGACTATTTTCTCATT 550
TTCTTTATCTTTTTCTCAATTTGTGGCAGACAAGTGAGGAGGCCCTG 600
TAATTGATTCATGCTTTTGCTTTCTTGACTTTTTGGAACAATACTATGCA 650
TCATATTTGGTCTTAATTATTCCTCTGTTTATTTCCAGAATTTTGAGCTC 700
TATACATCTAATAACAAAGCAAGCAGAGGATATATAGTTTCATCACTAA 750
AAAGGTTAGTCAACTCATCTAATATTTGCTACTCTCATCTCTATTGAAGT 800
ACAGTTATGGAAGTAGAAGTGATGTAAGAAAAATGAAAGAACTTTAGT 850
AGGTTAGTTGGATCTAACAAAGAGAAAGGGAAATAAATTGCAGGAGAAAG 900
AGAGAGGTTAAATACTTACTCACACCACCGATTTACAACAAATCACTTAA 950
TTGTGGTTAGTTAATGTATACTTTCACCTCATTAAATTATTACTTACCCA 1000
TGATAAGTTGTATTAATTTGGTATTAATATCCGGTGCGGGTGAATTCTTA 1005
CCGGTGAGAGGGATGGGGTTGGAGAGTGTGGAGTGAACAGAAGCAGATG 1100
TTTTAGATTTTTTCTAAGATGACGAAAGATTCCCCCTCACTAATGAAAATA 1150
TATTACTATACGCTATTAGAGATAGAAAGGTTCCGGTACCAGTTGGTCTCG 1200
TTTCTGGATGAACCCCATTTTTACAAGTCATTTTCTTCAATTCAAATCGC 1250
AAGTGACCTTTATCATCTTCCACTAATTAAGTCCTCTTAAGTTCGCGTG 1300
AAAATAGTGAAATTATTGATTATTCTTATCATTTTCATCTTCTTTCTCCTG 1350
ATAAAGTTTATGTACTTTTTATGCATCAGGTCTTGAGAACTTGGAAGG 1400
AAAAGTAGAATCATGGAAAAACGAAAAGATAATGAAGAAGCAAACAAC TC 1450
ATTGGTATGTTATTTGATAGAGTGAAGTGTAAAGTATTGAATTGTAGATA 1500
TCATGTGGCTTTAAAAATTTGATATGTGTTATTTTGGCAGGAGTCATTTT 1550
CTGCTCTTCGCAAGGATGCTGCCAATGTTCTGGATTTCCTAGAGAGATTA 1600
AAGAATGAAGAAGATCAAAGGCTGTTGATGTGGATCTGATTGAAAGCCT 1650

Figure 13D (cont.)

GAAATTGAAGCTGACATTTATTTGTACATATGTCCAGCTTTCTTATTCCG 1700
ATTTGGAGAAGTTTGAAGATATAATGACTAGAAAAAGACAAGAGGTTGAG 1750
AATCTGCTTCAACCAATTTTGGATGATGATGGCAAAGACGTCGGGTGTAA 1800
ATATGTCTTACTAGCCTCGCCGGTAATATGGATGACTGTATAAGCTTGT 1850
ATCATCGTTCTAAATCAGATGCCACCATGATGGATGAGCAATTGGGCTTC 1900
CTCCTCTTGAATCTCTCTCATCTATCCAAGCATCGTGCTGAAAAGATGTT 1950
TCCTGGAGTGACTCAATATGAGGTTCTTCAGAATGTATGTGGCAACATAA 2000
GAGATTTCCATGGATTGATAGTGAATTGTTGCATTAAGCATGAGATGGTT 2050
GAGAATGTCTTATCTCTGTTTCAACTGATGGCTGAGAGAGTAGGACGCTT 2100
CCTTTGGGAGGATCAGGCTGATGAAGACTCTCAACTCTCCGAGCTAGATG 2150
AGGATGATCAGAATGATAAAGACCCCTCAACTCTTCAAGCTAGCACATCTA 2200
CTCTTGAAGATTGTTCCAACCTGAATTGGAGGTTATGCACATATGTTATAA 2250
AACTTTGAAAGCTTCAACTTCAACAGAAATTGGACGCTTCATTAAGAAGC 2300
TCCTGGAAACCTCTCCGGACATTCTCAGAGAATATCTGATTCATCTACAA 2350
GAGCATATGATAACTGTTATTACCCCTAACACTTCAGGGGCTCGAAACAT 2400
TCATGTCATGATGGAATTCCTATTGATTATTCTTTCTGATATGCCGCCCA 2450
AGGACTTTATTATCATCATGACAACTTTTTGATCTCTTGGCTCGTGTGTGA 2500
GCAC TTACCAGGGAGGTATCAACTCTTGTACGCGACTTGAAGAGAAATT 2550
AAGGATTAAAGAGAGTACTGACGAAACAAATTGTGCAACCCATAAGTTTC 2600
TGGAATAATATTGAACTCCTTAAGGAAGATCTCAAACATGTTTATCTGAAA 2650
GTCCCGGATTCTATCTCAATATTGCTTCCCCATGAGTGATGGACCTCTCTT 2700
CATGCATCTGCTACAGAGACACTTAGATGATTTGCTGGATTCCAATGCTT 2750
ATTCAATTGCTTTGATAAAGGAACAAATTGGGCTGGTGAAAGAAGACTTG 2800
GAATTCATAAGATCTTTTTTCGCGAATATTGAGCAAGGATTGTATAAAGA 2850
TCTCTGGGAACGTGTTCTAGATGTGGCATATGAGGCAAAAGATGTCATAG 2900
ATTCAATTATTGTTTCGAGATAATGGTCTCTTACATCTTATTTTCTCACTT 2950
CCCATTACCAGAAAGAAGATGATGCTTATCAAAGAAGAGGTCTCTGATTT 3000
ACATGAGAACATTTCCAAGAACAGAGGTCTCATCGTTGTGAACCTCTCCCA 3050
AGAAACCAGTTGAGAGCAAGTCATTGACAAC TGATAAAATAATTGTAGGT 3100
TTTGGTGAGGAGACAACTTGATACTTAGAAAGCTCACCAGTGGACCGGC 3150
AGATCTAGATGTCATTTGATCATTTGGTATGCCGGGTTTAGGTAAACTA 3200
CTTTGGCGTACAAAGTATACAATGATAAATCAGTTTCTAGCCATTTTCGAC 3250
CTTCGTGCATGGTGCACGGTCGACCAAGTATATGACGAGAAGAAGTTGTT 3300
GGATAAAATTTTCAATCAAGTTAGTGACTCAAATTCAAAATTGAGTGAGA 3350
ATATTGATGTTGCTGATAAACTACGGAAACAATTGTTTGAAAGAGGTAT 3400

Figure 13D (cont.)

CTTATTGTCTTAGATGACGTGTGGGATACTAATACATGGGATGAGCTAAC 3450
AAGACCTTTTCCTGATGGTATGAAAGGAAGTAGAATTATTTTGACAACTC 3500
GAGAAAAGAAAGTTGCTTTGCATGGAAAGCTCTACACTGATCCTCTTAAC 3550
CTTCGATTGCTAAGATCAGAAGAAAGTTGGGAGTTATTAGAGAAAAGGGC 3600
ATTTGGAAACGAGAGTTGCCCTGATGAACTATTGGATGTTGGTAAAGAAA 3650
TAGCCGAAAATTGTAAAGGGCTTCCTTTGGTGGTGGATCTGATTGCTGGA 3700
ATCATTGCTGGGAGGGAAAAGAAAAGAGTGTGTGGCTTGAAGTTGTAAA 3750
TAATTTGCATTCTTTTATTTTGAAGAATGAAGTGAAGTGATGAAAGTTA 3800
TAGAAATAAGTTATGACCACTTACCTGATCACCTGAAGCCATGCTTGCTG 3850
TACTTTGCAAGTGCGCCGAAGGACTGGGTAACGACAATCCATGAGTTGAA 3900
ACTTATTTGGGGTTTTGAAGGATTTGTGGAAAAGACAGATATGAAGAGTC 3950
TGGAAGAAGTGGTGAATAATTTATTTGGATGATTTAATTTCCAGTAGCTTG 4000
GTAATTTGTTTCAATGAGATAGGTGATTACCCTACTTGCCAACTTCATGA 4050
TCTTGTGCATGACTTTTGTGTTGATAAAAGCAAGAAAGGAAAAGTTGTGTG 4100
ATCGGATAAGTTCAAGTGCTCCATCAGATTTGTTGCCACGTCAAATTAGC 4150
ATTGATTATGATGATGATGAAGAGCACTTTGGGCTTAATTTTGTCTGTG 4200
CGGTTCAAATAAGAAAAGGCATTCCGGTAAACACCTCTATTCTTTGACCA 4250
TAAATGGAGATGAGCTGGACGACCATCTTCTGATACATTTTCATCTAAGA 4300
CACTTGAGGCTTCTTAGAACCTTGACCTGGAATCCTCTTTTATCATGGT 4350
TAAAGATTCTTTGCTGAATGAAATATGCATGTTGAATCATTTGAGGTACT 4400
TAAGCATTGGGACAGAAGTTAAATCTCTGCCTTTGTCTTTCTCAAACCTC 4450
TGGAATCTAGAAATCTTGTGTTGTGGATAACAAAGAATCAACCTTGATACT 4500
ATTACCAGAATTTGGGATCTTGTAAGTTGCAAGTGCTGTTACGACTG 4550
CTTGTTCTTTCTTTGATATGGATGCAGATGAATCAATACTGATAGCAGAG 4600
GACACAAAGTTAGAGAACTTGACAGCATTAGGGGAACCTCGTGCTTTCTTA 4650
TTGGAAAGATACAGAGGATATTTTCAAAGGCTTCCCAATCTTCAAGTGC 4700
TTCATTTCAAACCTCAAGGAGTCATGGGATTATTCAACAGAGCAATATTGG 4750
TTCCCGAAATTGGATTTCTTAACCTGAAGTGAAGAACTCACTGTAGATTT 4800
TGAAAGATCAAACACAAATGACAGTGGGTCTCTGCAGCCATAAATCGGC 4850
CATGGGATTTTCACTTTCTTCGAGTTTGAAAAGATTGCAATTGCATGAA 4900
TTTCTCTGCATCCGATTCATCTATCAACAATAGCGAGACTGCTGAACCT 4950
TGAAGAGTTGTACCTTTATCGTACAATCATCCATGGGGAAGAATGGAACA 5000
TGGGAGAAGAAGACACCTTTGAGAATCTCAAATGTTTGATGTTGAGTCAA 5050
GTGATTCCTTCCAAGTGGGAGGTTGGAGAGGAATCTTTTCCACGCTTGA 5100
GAAATTAGAACTGTCGGACTGTCATAATCTTGAGGAGATTCCGTCTAGTT 5150

Figure 13D (cont.)

TTGGGGATATTTATTCCTTGAAAATTATCGAACTTGTAAGGAGCCCTCAA 5200
CTTGAAAATTCGCTCTCAAGATTAAGGAATATGCTGAAGATATGAGGGG 5250
AGGGGACGAGCTTCAGATCCTTGGCCAGAAGGATATCCCGTTATTTAAGT 5300
AGTTTTTTGAGCATTATGGTTGAAAAGTAGATTGCACTTTGCTGGGTAGAT 5350
TGTATATGGTTAAGAAAATTCTGTTACAGTTGTTATGAAACATTTTTATT 5400
TGACTTTTCTGAGTTTCTTTTAGAAAACCTCAGAAGTTTTTAACAAAAATT 5450
ATAGTTTTTATAAATACAATGTGGATTGTCCTTTGGCTGTCCAACCTGGT 5500
CTGAAGTCTCATATGCTCAGAGCACTATCGTTCAACCTCAATCAAGGTAC 5550
TGATTTAAATGACATCTATACTACTTTATCACAACCCAACGAACTTTC 5600
ATCTCAAAAGCTAGGCCAGGAAGTGAAGAGTTGTAGAGAGCTTATAAGC 5650
ACTCATGACTTCCTTTTCTCGAACATTCAACCAACGTAGGCTGAAATCCC 5700
ACTCTGAACGAAAATAAGTGTTTGTATTCAAATTAACCTCTCGTAGTAGA 5750
ACACTGAAATACCTTCTCTAAACGTTCAACAAATGGGATTTCCAGCACT 5800
CAAAGTGAATGAAAGGTTACATTAACTTCAAAAAGAATTACGACAATT 5850
CATGACCACAAGTACATTGACAGCACCATTTCAACAGAAGAACAAGTCAA 5900
TGCTGCATCTTCATCAATAATCCGAGTGTGGAACCTCCTTCCTGCACTG 5950
TCCTGTATATGTAAAGTTTCTCAACAGGGCAACTTTCTGGTCTCGTATCT 6000
GGATGACCCCTCTCGTCTATAACTTCAACATTAAGCCCTGGCAACTTCTG 6050
GACCAACAGCTTACATGCTTCAAACTTACTGAACAATTAGACATCCAAA 6100
GGGATCGCATTGTCTCCAGCTTTGCAGCATTAGCCAACAGAGCCTCATCG 6150
CCAAAGGGGCAGTCTCTAATCTCGAATTTGAAAAAATTGTTGTTGTATGA 6200
CTTTCCTCTGACATCCGATGCACTATCAACAATAGCAAGACTGGAGGTTG 6250
GAGAGGAATCCTTTATTATACAATCATTCAGGGAGAAGAATGGAACATGG 6300
GGGAGGAAGACACTTTTGAGAATCTGAAATGTGTTAGAGCCACAAGCTAC 6350
AGAAGTATTGAATTTGTCATGAATATCAACATTCTTCATCCTAGTTAATT 6400
CTTTTTCAATTTTTAATAGACTCTCATTTTAATCACTAATATTCTTCTAT 6450
TTGTGACTTCTTTTCTGCAGGTGGCAACTTTAAATTCATAAAGTATAGGA 6500
TTGATGACAACTCGAAAAATATCTTAATGAGGTGAAGTTTGAGCAGTCA 6550
GCAGATGGTGGTTCCAACCTCTAAGTTGACAAGCACATACTATCCCGGAGG 6600
GCGATTTCAAGCCTGATGCATATGGTTAGTGTGGCTAGAGCAGACAGGAT 6650
GTATTACCTGGATATCTACCAAGACGAATCCACAATCAGTTTTATGTCAA 6700
GCAATACATGAAGTAACTCCCGATAGAACAGTAAAAGCAAGATGTGTAGG 6750
TGTATCTCGACTCTAAGAGATTGTACATTCTCTTTGAGATTTTTACTGC 6800
TAATACAAATTTACACCTCAGAAGCGAATCTAGAATTTCTAGAGCATGAA 6850
TGCACCACTAATGAAAGGAGAAAAAAGGAAGTATGAAGTGGGAATTTGAT 6900

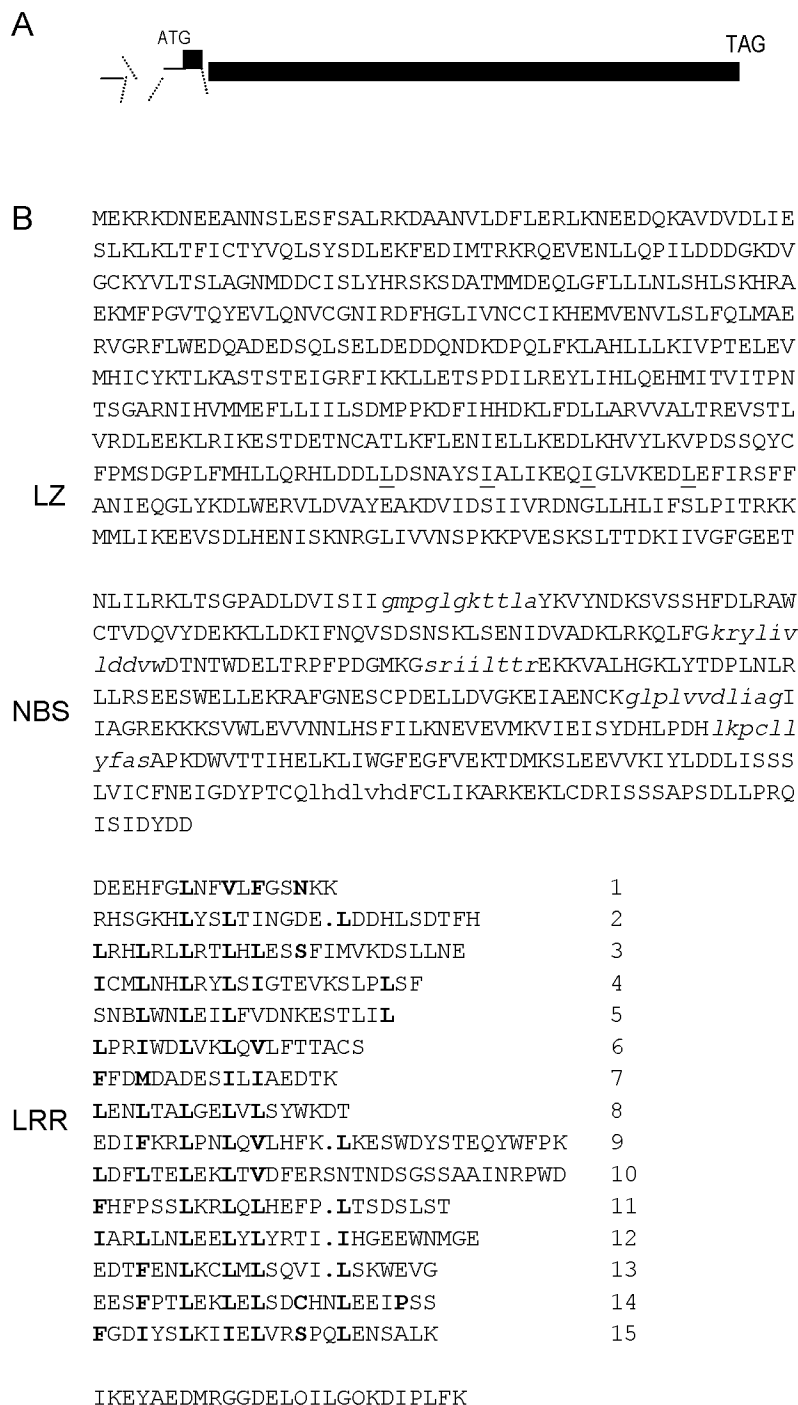
Figure 13D (cont.)

CCTTGTTTCTAGGTATATAAAATTTATCATTCAACTATACTTCATTTAGC 6950
AAACAACCTCTCTTTGCCATTATTTCTCAAACAAGGGCTTCTAATATTGCT 7000
AAACTAAAGACTGTCAAAGGTAAGTTCATCTTCAAACCTCTCTTGTTTAC 7050
TTTATCTAAAGGGGAACATGAAAAACAAGAAACATCAGGAATGTCCCGT 7100
AAACAAAGCAGCCTCATGCACAAAACATCCAACGTTGGTAGGATTAATGG 7150
AGGGATCGCATCCCAGGAGGATACTGTAGAAAAATTAGTGGCTTCTTTCA 7200
CCGCTCAAACCCATGATCTATAGGTTACATGGAGACAACTTTATGGTTGC 7250
TCGTAGGCTCCCGTCAATTCTCATAAACCACAACACCAAAGTTGCATCAG 7300
ACATCATCTTCATTACAAAGCTGACAATCTCCACAAGTCTTAGTCAACTT 7350
GTAATATGAATATTAGCCAGGTAGACGTACATATTTACAAAATTGAGTTT 7400
CCTATATAATATGGTTTGAAGGAATGAAACATGATGGGGAGGGTAGATAA 7450
AATAATATATGAGGCATAAAAAATAGGAAAGATATTTGTAGTGAGAGGTTT 7500
TGACTTTTTATGCTGCTTTTGATCTTCAGTTTCTTGTATTCTTTTTCTAC 7550
TGCTTTCTCTTCTTTCTCCTGAGTAAAGTTTTATGTAGGTACTTTTTAT 7600
ACGTCCGATCGTGAGAACTTGAAAGAAAGCTCTCTATAGCTATGTTAGGT 7650
GCCCACATAAAAAAATGAAATATTACAAAACCCTGATAATAAAATACAC 7700
TAATCTAAGATATTCAC TGCAACATACATGCAAAATATATATATATAAAT 7750
TTTCATGAAAATTATAACAAATAATAGATGTGAACATATAACTTTAAAAA 7800
TAATATTACATCCATAAAGCTTAAATTCTAGATCCATCTATGCTTGTATG 7850
ATGCATAGCTCAGAATATCTCCATCAAGTGTTAAACTACATATTTCATTC 7900
AAATTTATATAGAAAACGATAATTAAGGTGAAAACTTTATAAAGATATC 7950
GTGTGGTTGTGTGAGTGAGGTGACAAAATAAGTTGTGTGATTATTCAAAA 8000
AGTTTTTAATAACGAAAATCCACATGCTTGAATTAATTGAAGCATTAAATGT 8050
TGTAACGAAAAATATTACATTTATTGAGTTACTGTGATGTTTTAACTGAT 8100
ATATAAAATAATATTGGTATTTCTCTTCATCTGCGACATAATATGTTTTT 8150
TCATCTTTTTTCAATATACAAAATAGAATTATTATTTTGTGTCATCTTTT 8200
TAAGTACAAATATTTCATATGTATATAGTACAAAATAAAATATTTACTGT 8250
GGTAAAGTAAATGGAATAAGAGGTCATATTTGAAATAACAATATACTATA 8300
CTATGTTAAAGTATTTTTTATAGTTAAAATTTCTCTAGAGTACTTGATTC 8350
TACATACAAATACTAATTTTCGTAAAAAATTAATATTGAATTTCTTCATT 8400
GTTTCTTTATTATTAAATTAGTTTATAATAACTAACTAAGGTAATAAGA 8450
CCTTAGTTTAGTTAATGTGTGTCTCTGTGATTTTCGTTTCATAGTCTAAGGG 8500
TGTACTTGTGCCTTATCCCAAAAATGAAGGAATATCAAAGATATATTAA 8550
AATTAAATTAAATATTTGGAGGTTATGAATATAAAAAGTATCAGAGTTCT 8600
ACATATAAAGAGTAACAATTGAAATAATTAATTAATATGAGATATGAAG 8650

Figure 13D (cont.)

GCGGACATTTAAAGAAAATAATAAATAAATAAATTAAAGGGTATAAATTT 8700
CATAATACATAATACCAATAAGCCGTAGAATATCTCCGTCATAATGCATA 8750
AACTAATAAATCACAAATGTATAACTCACATACAAATATTTTTTGATAAA 8800
GAATTTGAATGTTGTAATAGAATGGAGAATAACTTGTGTCTTATTCATT 8850
ATGTAAGACGTATAAATACAAATACAATGAGCTCTAATTAATTAAGGAAA 8900
CTAAATAAGGAAGGAATCAAAAAATATTATGTCATATCCCTACATATCTG 8950
CTAGAGATTCTATCATATCCTTACATATCTGTTAAGCTATGTCTACACCT 9000
AAAGGTGTCTACAATCATTTTGTAACTCCCCCTCAAGTTAGAGCATAG 9050
ATATTATTCATTCCCAACTTGTTACAAAGATAATCAACTCGAGTTCATT 9100
CAACGCTTTTGTGAACAAATCAACTAGTTGCTCTCCTGTCTTCACTTAGC 9150
TAGTGGATATCAGGTTTTTCATGAATCTTCTCACGAATAAAATGACAGTCA 9200
ACCTCAATATGTTTAGTTCTTTCATGAGACACCGGATTCAAGGCAATATG 9250
GAGCGCAACTTGATTATCATACTAGAGTTTTGATGGTATATGATGCTTCA 9300
ACCCTATTTCTGTTAAAAGATAATGTATCCACATGATCTCACCCATAGAC 9350
TGTAACATAACTCTGTACTTTGATTCTGCACTAGATCAAGATACAACATT 9400
TTGCTTTTTACTCCTCCATGATACCAGGTTTCATCCAACAAAGACACAAT 9450
AACTTGTTAGTAGATCTTCTATCAATTTTCGATCCAGCCCAATCGACATCT 9500
GCAAAACACTCAATATGAGTATGGTCGTGATTTTGATACTATATTCCAAG 9550
ACTAGGAGTTTTCTTCAAGTAACATAGAATATGTTCCAAAGCTGCCAGT 9600
GTTTGACGTAGGTGCAAACATGAAC TAGCTAACAACACTTACTGCAAAAG 9650
CAATATCAAGATGAGTCACAATAAGGTAGTTTAACTTTCCAAC TAACCTT 9700
TTGTATCTCTATGGATCATTAAGGATCGTCGTCATCTTTCATAAGATG 9750
CATATTGGGAACCATTGGAAGTTCAGGGTTTGGCTGCCATCTTCAAT 9800
TTTCTGCAAGTAGATCGAGAGAATATATTCTCTAAGACAAAAGAATTCCC 9850
TTTTTGTTTCTATTTACTTCTACTCCCAAAATGTATTTCAATTGACCCAA 9900
GTCCTTCGTATGAAACCAAGTATGCAGGAAAGACTTGAGGGAAGAGATC 9949

Figure 14



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Mil.1 57	VL	S	I	D	V	---	N	L	K	Q	V	KI	MA
Mil.2 57	I	VL	S	I	I	---	N	L	K	Q	V	KL	MA
Rpi-blb2 60	MEKRKDNEEANNLSLESPSALAKDAANVLDFLERLKNEDQKAVDVDLIESLKLKLTFFICT												
Mil.1 109	C	F	Q				L	-----	F			TS	
Mil.2 109	Y	F	Q		N		SL	-----				TS	
Rpi-blb2 120	YVQLSYSDLERKFEDIMTRKRQEVENLLQPIILDDDGKDVGCKYVLTSLAGNMDDCISLYHR												
Mil.1 169	Y	I		D		Y	H	I				I	G
Mil.2 169	Y	I		D		Y	H	I					L G
Rpi-blb2 179	S-KSDATMMDEQLGFLLLNLSHLSKHRAEKMFPGVTQYEVQLQNVCGNIRDPHGLIVNCCI												
Mil.1 229		P		D	H	D	T	R		E	R	SR	
Mil.2 229		P			H		T	R		EH	R	SR	Q T
Rpi-blb2	KHEMVENVLSLFLQMAERVGRFLWEDQADEDSQLSELDEDDQNDKDPQLFKLAHLKLLKIV 239												
Mil.1 289	V	I		TN		A	V	L	Q		P	V	S
Mil.2 289				TN		A	V				I	Q	L P S L
Rpi-blb2 299	PTELEVMMHICYKTLKASTSTEIGRFIXKLLLETSPDILREYLIHLQEHMITVITPNTSGAR												
Mil.1 348		L		-				D	GV			EP	N GNNQ
Mil.2 348		L		-				H	GT			N	GNNQ
Rpi-blb2 359	NIHVMMEFLLIILSDMPPKDFIHDKLFDLLARVVALTREVSTLVRDLEEKLRKESTDE												
Mil.1 408	DL			K		AL		C				HI	N
Mil.2 408	DL			K		A	N	C				HM	N
Rpi-blb2 419	TNCATLKFLENIELLKEDLKHVYLKVPDSSQYCFPMSDGPLFMHLLQRHLDLDDLSNAYS												
Mil.1 467		E	E	Q	K		VD-A		A				
Mil.2 468	S		E	E	SQE		GDA		I	A			
Rpi-blb2 478	IALIKEQIGLVKEDLEFIRSFAN-IEQGLYKDLWERVLDVAYEAKDVIDSIIVRDNGLL												
Mil.1 527		I	IK			I	A	D	P	D		R	T E
Mil.2 528		I	IK			I	A	D	P	D		R	I E
Rpi-blb2 538	HLIFSLPITRKKMLIKEEVSDLHENISKNRGLIVVNSPKKPVESKSLTTDKIIVGFGE												
Mil.1 587		S			T	S					R		GC

FIGURE 15

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Mil.2		T	S		R		G	D
588								
Rpi-blb2	TNLILRLKLTSGPADLDVISII	gmpg	lgktt	lay	KVYNDKSVSSHFDLRAWCTVDQVYDEK			
598								
Mil.1	NT	S	D			T		ESK
647								
Mil.2	T	S	G	D	N	T	L	EAK
648								
Rpi-blb2	RLLDKIFNQVSDSNSKLS	ENIDVADKL	RKQLFGK	ryli	vlddw	DTNTWDELTRPFPDGM		
658								
Mil.1		E	N	D	PD			
707								
Mil.2		E	N	D	PD	D	T	
708								
Rpi-blb2	KGSRIILT	TREKKVALH	GKLYT	PLNLRL	LSZESWELLEKRAFGN	ESCPDELLDVGKEI		
718								
Mil.1		A	V		R	QSS	S	NS
767								L
Mil.2		A	V		R	QSS	S	NS
768								L
Rpi-blb2	AENCKg	iplv	vdliag	IIAGREKK	KS	VWLEVVNNL	HSFILKNEVEVMK	VEISYDHL
778								PDH
Mil.1		F	TSL	Y	NVYF	A	G	ENM
827								M
Mil.2		H	W	TPL	YLFTVYL	A	E	GI
828								M
Rpi-blb2	lkpc	llyfas	APKDW	VTTI	HELKLI	WGFE	GVEKTD	MKSLEE
838								VVKIYLD
Mil.1		YALNF	I		N	F	Q	R
886								T
Mil.2		ILNF	I		N	F	R	
888								T
Rpi-blb2	NEIGDYPTC	Qihd	lvhd	FCLIKARKEK	LC	DRIS	SAPS	DL
898								PRQISIDYDDDEEHFGLNE
Mil.1		M	D		R	I	Q	SV
946								A
Mil.2		M	D		R	Q	SV	A
948								I
Rpi-blb2	VLEGS	NKKR	PHSGK	HL	SLT	INGDE	LD	DL
958								SDTFHLRHLRLRL
Mil.1		1		2			3	
1006			D	Q	Y		S	STNR
Mil.2							V	L
1008			R	R	Q	Y	F	
Rpi-blb2							S	S
1018							G	I
Mil.1							V	L
1066								R
Mil.2								S
1068								V
Rpi-blb2								L
1078								R
Mil.1								
1126								
Mil.2								
1128								

FIGURE 15 (cont.)

Rpi-blb2	STEQYWFPKLDFLTELEKLTVD EE RSNTNDSGSSAAINRPWDFHFPSSLKRLQLHEEPLT									
1138										
				10						11
Mil.1		P		S	H			F	NFN	SI
1186										
Mil.2		P		N	S	D	Q		F	N RLLT
1188										
Rpi-blb2	SDSLSTIARLLNL EELY LXRTIIHGEEWNMGEEDTFENLXCI ML SOVILSKWEVGEESFP									
1198										
				12					13	
Mil.1	N	K	RG	K	P			S	KI	K D
1246										
Mil.2	N	K	QE	GK	P			F	KI	K D K ND
1248										
Rpi-blb2	TLEKLELSDCHNLEEIPSSF GD IYSLK IT ELVRSPOLENSALKIKEYAEDMRGGDELQIL									
1258										
				14					15	
Mil.1	N									1255
Mil.2	N									1257
Rpi-blb2	GQK	D	I	P	L	F	K			1267

FIGURE 15 (cont.)

Figure 16: Multiple Sequence Alignments of Mi1.1, Mi1.2 and Rpi-blb2 nucleic acids

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CIUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: Mi1.1          3768 bp
Sequence 2: Mi1.2          3774 bp
Sequence 3: Rpi-blb2       3804 bp
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 95
Sequences (1:3) Aligned. Score: 89
Sequences (2:3) Aligned. Score: 89
Guide tree      file created: [/ebi/externserv/clustalw-
work/interactive/clustalw-20040503-14435620.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences:  2      Score:68908
Group 2: Sequences:  3      Score:65855
Alignment Score 66872
CLUSTAL-Alignment file created [/ebi/externserv/clustalw-work/interactive/clustalw-
20040503-14435620.aln]

CIUSTAL W (1.82) multiple sequence alignment

Mi1.1      ATGGAAAAACGAAAAAGATAATGAAGAAAGCAAAACAACTCATTGGTGCTATTTTCTGCTCTT  60
Mi1.2      ATGGAAAAACGAAAAAGATAATGAAGAAAGCAAAACAACTCATTGGTGCTATTTTCTGCTCTT  60
Rpi-blb2   ATGGAAAAACGAAAAAGATAATGAAGAAAGCAAAACAACTCATTGGAGTCATTTTCTGCTCTT  60
*****

```

Figure 16 (cont.)

```
Mi1.1      AGCAAGGACATTGCCGATGTTCTGGTTTCTCTAGAGA-----ATGAGGAAAAATCAA 111
Mi1.2      AGCAAGGACATTGCCAATGTTCTAAATTTCTCTAGAGA-----ATGAGGAAAAATCAA 111
Rpi-blb2   CGCAAGGATGCTGCCAATGTTCTGGATTTCTTAGAGAGATTAAAGAATGAAGAAGATCAA 120
          *****  ****  *****  ****  ****  *****
Mi1.1      AAAGCTCTTGACAAAAGATCAAGTTGAAAAAGATAAAATTGAAAAATGGCAATTATTTGTACA 171
Mi1.2      AAAGCTCTTGACAAAAGATCAAGTTGAAAAAGCTAAAAATGAAAAATGGCAATTATTTGTACA 171
Rpi-blb2   AAGGCTGTTGATGTGGATCTGATGTGAAGCCTGAAATTTGAAGCTGACATTTATTTGTACA 180
          ** *** ****  ****  *****  * ***** ** *****
Mi1.1      TATGTTTCAGCTTTCTTTGTTCCGATTTTGAGCAGTTTGAAGATATAATGACTAGAAAAAGA 231
Mi1.2      TATGTTTCAGCTTTCTTTATTTCCGATTTTGAGCAGTTTGAAGATATAATGACTAGAAAAAGA 231
Rpi-blb2   TATGTTCCAGCTTTCTTTATTTCCGATTTTGGAGAAAGTTTGAAGATATAATGACTAGAAAAAGA 240
          *****  *****  *****  ***  ***** ***** *****
Mi1.1      CAAGAGGTTGAGAAATCTGCTTCAACCACTTTTGGATGATGATG----- 274
Mi1.2      CAAGAGGTTGAGAAATCTGCTTCAATCACTTTTGGATGATGATG----- 274
Rpi-blb2   CAAGAGGTTGAGAAATCTGCTTCAACCAATTTTGGATGATGATGCGCAAGACGTCGGGTGT 300
          ***** ***** ***** ** *****
Mi1.1      -----TCCTTTACTAGCCTCACCAAGTAATATGGATGACTGTATCAGCTTGATCATCGT 327
Mi1.2      -----TCCTTTACTAGCCTCACCAAGTAATATGGATGACTGTATCAGCTTGATCATCGT 327
Rpi-blb2   AAATATGTCCTTACTAGCCTCGCCGTAATATGGATGACTGTATAAGCTTGATCATCGT 360
          ** ***** ** ***** ***** *****
Mi1.1      TCTTATAAATCAGATGCCCATCATGATGGATGAGCAATTGGACTTCCTCCTCTTGAATCTC 387
Mi1.2      TCTTATAAATCAGATGCCCATCATGATGGATGAGCAATTGGACTTCCTCCTCTTGAATCTG 387
Rpi-blb2   TCT---AAATCAGATGCCCATCATGATGGATGAGCAATTGGGCTTCCTCCTCTTGAATCTC 417
          *** ***** ***** ***** ***** ***** *****
```

Figure 16 (cont.)

Mi1.1	TATCATCTATCCAAGCATCAGGCTGAAAAAGATATTTCCCTGGAGTGACTCAATATGAAGTT	447
Mi1.2	TATCATCTATCCAAGCATCAGGCTGAAAAAGATATTTCCCTGGAGTGACTCAATATGAAGTT	447
Rpi-blb2	TCTCATCTATCCAAGCATCGTGCCTGAAAAAGATGTTTCCCTGGAGTGACTCAATATGAAGTT	477
	* ****	
Mi1.1	CTTCAGAAATATATGTGGCAACATAAAGAGATTTCCATGGGTTGATAGTGAATGGTTGCATT	507
Mi1.2	CTTCAGAAATGATGTGGCAACATAAAGAGATTTCCATGGGTTGATAGTGAATGGTTGCATT	507
Rpi-blb2	CTTCAGAAATGATGTGGCAACATAAAGAGATTTCCATGGGTTGATAGTGAATGGTTGCATT	537

Mi1.1	AAGCATGAGATGGTTGAGAAATGTCCTTRCCTCTGTTTCAACTCATGGCTGACAGAGTAGGA	567
Mi1.2	AAGCATGAGATGGTTGAGAAATGTCCTTACCTCTGTTTCAACTCATGGCTGAAAGAGTAGGA	567
Rpi-blb2	AAGCATGAGATGGTTGAGAAATGTCCTTATCTCTGTTTCAACTCATGGCTGAGAGAGTAGGA	597

Mi1.1	CACCTCCTTTGGGATGATCAGACTGATGAAGACTCTCGACTCTCCGAGCTAGATGAGGAT	627
Mi1.2	CACCTCCTTTGGGAGGATCAGACTGATGAAGACTCTCGGCTCTCCGAGCTAGATGAGGAT	627
Rpi-blb2	CGCTTCCTTTGGGAGGATCAGGCTGATGAAGACTCTCAACTCTCCGAGCTAGATGAGGAT	657
	* ****	
Mi1.1	GAACAAAAATGATAGAGACTCTCGACTTTTCAAGCTAGCACATCTACTCTTGAAGATCGTT	687
Mi1.2	GAACACAAATGATAGAGACTCTCGACTCTTCCAGCTAACACATCTACTCTTGAAGATGTT	687
Rpi-blb2	GATCAGAAATGATAAAGACCCCTCAACTCTTCAAGCTAGCACATCTACTCTTGAAGATGTT	717
	** **	
Mi1.1	CCGGTGAACCTGGAGGTTATACACATATGTTATACAAACTTGAAAGCTTCAACTTCAGCT	747
Mi1.2	CCAACTGAACCTGGAGGTTATGCACATATGTTATACAAATTTGAAAGCTTCAACTTCAGCA	747
Rpi-blb2	CCAACTGAATGGAGGTTATGCACATATGTTATATAAACTTTGAAAGCTTCAACTTCACA	777
	** ****	
Mi1.1	GAAGTTGGACTCTTCAATTAAGCAGCTTCTAGAAACCTCTCCAGATATCTTGAGGGAATAT	807

Figure 16 (cont.)

Mi1.2	GAAGTTGGACGCTTCATTAAAGAGCTCCTGGAAACCTCACCGGATATTCACAGAGAAATAT	807
Rpi-blb2	GAAATGGACGCTTCATTAAAGAGCTCCTGGAAACCTCTCGGACATTCACAGAGAAATAT	837
	*** ****	
Mi1.1	CTAATTCCTCTGCAAGAGCACATGGTAACGTATTATACCCCTAGCACCTCAGGGGCTCGA	867
Mi1.2	ATCATTCAACTACAAGAGCATATGTTAACTGTTATTCCCCCTAGCACCTTAGGGGCTCGA	867
Rpi-blb2	CTGATTCATCTACAAGAGCATATGATAACTGTTATTACCCCTAACACTTCAGGGGCTCGA	897
	* **** ** ****	
Mi1.1	AACATTCATGTCATGATGGAATTCCTATTACTTATCTTTCTGATATGCC---	924
Mi1.2	AACATTCATGTCATGATGGAATTCCTATTACTTATCTTTCTGATATGCC---	924
Rpi-blb2	AACATTCATGTCATGATGGAATTCCTATTGATTATCTTTCTGATATGCCGCCCAAGGAC	957

Mi1.1	TTTATTCATCATGACAAACTTTTGTATCTCTTGGATCGTGTGGAGTACTTACCAGGGAG	984
Mi1.2	TTTATTCATCATGACAAACTTTTGTATCTCTTGGCTCATGTTGGAACACTTACCAGGGAG	984
Rpi-blb2	TTTATTCATCATGACAAACTTTTGTATCTCTTGGCTCGTGTGTAGCACTTACCAGGGAG	1017

Mi1.1	GTATCAACTCTTGTACGTGACTTGGAAAGAGGAACCAAGGAATAAAGAGGGTAATAACCAA	1044
Mi1.2	GTATCGACTCTTGTACGTGACTTGGAAAGAGAAAATTAAGGAATAAAGAGGGTAATAACCAA	1044
Rpi-blb2	GTATCAACTCTTGTACGCGACTTGGAAAGAGAAAATTAAGGATTAAGAGAGTACTGACGAA	1077

Mi1.1	ACAAAATTGTGCAACCCCTAGACTTGTCTGGAAAAATATTGAACCTCCTCAAGAAAAGATCTCAA	1104
Mi1.2	ACAAAATTGTGCAACCCCTAGACTTGTCTGGAAAAATATTGAACCTCCTCAAGAAAAGATCTCAA	1104
Rpi-blb2	ACAAAATTGTGCAACCCCTAAAGTTCTTGGAAAAATATTGAACCTCCTTAAGGAAAGATCTCAA	1137

Mi1.1	CATGTTTATCTGAAAAGCCCTGGATTTCATCTCAATGTTGCTTCCCCCATGATGGACCA	1164
Mi1.2	CATGTTTATCTGAAAAGCCCAATTCATCTCAATGTTGCTTCCCCCATGATGGACCA	1164

Figure 16 (cont.)

Rpi-blb2	CATGTTTATCTGAAAGTCCCGGATTCACTCAATATTGCTTCCCCATGATGATGGACCT 1197 ***** ** *****
Mi1.1	CTCTTCATGCATCTTCTACACATACACTTAAATGATTTGTTAGATTCCTAATGCTTATTCA 1224
Mi1.2	CTCTTCATGCATCTTCTACACATGACCTTAAATGATTTGCTAGATTCCTAATGCTTATTCA 1224
Rpi-blb2	CTCTTCATGCATCTGCTACAGAGACACTTAGATGATTTGCTGGATTCCTAATGCTTATTCA 1257 ***** * ***** * ***** * ***** * *****
Mi1.1	ATTGCTTTGATAAAGGAAGAAATCGAGCTGGTGAAGCAAGACCTGAAATTCATAAGATCA 1284
Mi1.2	ATTCTTTTGATAAAGGAAGAAATCGAGTTGGTGAGTCAAGAACTGGAATTCATAAGATCA 1284
Rpi-blb2	ATTGCTTTGATAAAGGAACAAATTGGGCTGGTGAAAGAAAGACTTGGAATTCATAAGATCT 1317 *** ***** * * ***** * ***** * *****
Mi1.1	TTCTTTTGTTGGATGCTG---AGCAAGGATTGTATAAAGATCTCTGGGCACGTGTTCTAGAT 1341
Mi1.2	TTCTTTGGGGATGCTGCTGAGCAAGGATTGTATAAAGATATCTGGGCACGTGTTCTAGAT 1344
Rpi-blb2	TTTTTCGCGAATATTG---AGCAAGGATTGTATAAAGATCTCTGGGAACGTGTTCTAGAT 1374 ** ** * ** ** ***** ***** * ***** * *****
Mi1.1	GTGGCTTATGAGGCAAAAGATGTCTATAGATTCAATTATTGTTTCGAGATAATGGTCTCTTA 1401
Mi1.2	GTGGCTTATGAGGCAAAAGATGTCTATAGATTCAATTATTGTTTCGAGATAATGGTCTCTTA 1404
Rpi-blb2	GTGGCATATGAGGCAAAAGATGTCTATAGATTCAATTATTGTTTCGAGATAATGGTCTCTTA 1434 ***** ***** ***** ***** ***** ***** *****
Mi1.1	CATCTTATTTCTCACTTCCCATACCATAAAGAAGATCAAACTTATCAAAGAAGAGATC 1461
Mi1.2	CATCTTATTTCTCACTTCCCATACCATAAAGAAGATCAAACTTATCAAAGAAGAGATC 1464
Rpi-blb2	CATCTTATTTCTCACTTCCCATACCAGAAAGAAGATGATGCTTATCAAAGAAGAGGTC 1494 ***** ***** ***** ***** * ***** ***** *
Mi1.1	TCTGCTTTAGATGAGAACATTCCCAAGGACAGAGGTC TAATCGTTGTGAACTCTCCCAAG 1521
Mi1.2	TCTGCTTTAGATGAGAACATTCCCAAGGACAGAGGTC TAATCGTTGTGAACTCTCCCAAG 1524
Rpi-blb2	TCTGATTTACATGAGAACATTTCCAAGAACAGAGGTC TCATCGTTGTGAACTCTCCCAAG 1554

Figure 16 (cont.)

```

**** **** ***** ***** ***** ***** ***** *****
Mi1.1 AAACCAGTTGAGAGAAAAGTCATTGACAACTGATAAAAATAACTGTAGGTTTGAGGAGGAA 1581
Mi1.2 AAACCAGTTGAGAGAAAAGTCATTGACAACTGATAAAAATAATGTAGGTTTGAGGAGGAG 1584
Rpi-blb2 AAACCAGTTGAGAGCAAGTCATTGACAACTGATAAAAATAATGTAGGTTTGAGGAGGAG 1614
***** ***** ***** ***** ***** ***** ***** *****
Mi1.1 ACAAACTTGATACTTAGAAAGCTCACCAAGTCAGAGTGGATCGGCAGATCTAGATGTCATTTTCGATC 1641
Mi1.2 ACAAACTTGATACTTAGAAAGCTCACCAAGTCAGAGTGGATCGGCAGATTTAGATGTCATTTTCGATC 1644
Rpi-blb2 ACAAACTTGATACTTAGAAAGCTCACCAAGTCAGAGTGGATCGGCAGATCTAGATGTCATTTTCGATC 1674
***** ***** ***** ***** ***** ***** ***** *****
Mi1.1 ACTGGTATGCCGGGTTCAGGTAAAACACTACTTTTGGCATACAAAAGTATACAATGATAAGTCA 1701
Mi1.2 ACCGGTATGCCGGGTTCAGGTAAAACACTACTTTTGGCATACAAAAGTATACAATGATAAGTCA 1704
Rpi-blb2 ATTGGTATGCCGGGTTTAGGTAAAACACTACTTTTGGCGTACAAAAGTATACAATGATAAGTCA 1734
* ***** ***** ***** ***** ***** ***** ***** *****
Mi1.1 GTTTC TAGCCGTTTCGACCTTCGTGCATGGTGCACGGTCGACCAAGGATGTGATGAGAAG 1761
Mi1.2 GTTTC TAGACATTTTGACCTTCGTGCATGGTGCACGGTCGATCAAGGATATGACGACAAG 1764
Rpi-blb2 GTTTC TAGCCATTTTCGACCTTCGTGCATGGTGCACGGTCGACCAAGTATATGACGAGAAG 1794
***** * *** ***** ***** ***** ***** ***** ***** *****
Mi1.1 AAGTTGTTGAATACAAATTTTCAGTCAAGTTAGTGACTCAGATTCAAATTCAGTGAGAAT 1821
Mi1.2 AAGTTGTTGGATACAAATTTTCAGTCAAGTTAGTGGCTCAGATTCAAATTCAGTGAGAAT 1824
Rpi-blb2 AAGTTGTTGGATAAAAATTTTCATCAAGTTAGTGACTCAAAATTCAAATTCAGTGAGAAT 1854
***** ***** ***** ***** ***** ***** ***** ***** *****
Mi1.1 ATTGATGTTGCTGATAAAATTACGGAAACAACACGTTTGGAAAAGAGGTATCTTATGTCTTA 1881
Mi1.2 ATTGATGTTGCTGATAAAATTGCGGAAACAACACGTTTGGAAAAGAGGTATCTTATGTCTTA 1884
Rpi-blb2 ATTGATGTTGCTGATAAAACTACGGAAACAACATGTTTGGAAAAGAGGTATCTTATGTCTTA 1914
***** ***** ***** ***** ***** ***** ***** ***** *****
```

Figure 16 (cont.)

Mi1.1	GATGACGTGTGGGATACCTACATGGGATGAGTTAAACAAGACCTTTCCCTGAATCTAAG	1941
Mi1.2	GATGATGTGTGGGATACCTACATGGATGGATGAGTTGACAAGACCTTTCCCTGAAGCTAAG	1944
Rpi-blb2	GATGACGTGTGGGATACCTAAATACATGGGATGAGCTAACAAAGACCTTTCCCTGATGGTATG	1974
	*****	** *
Mi1.1	AAAGGAAGTAGGATTATTTTGACAACTCGGAAAAAGGAAGTGGCTTTGCATGGAAAAAGCTG	2001
Mi1.2	AAAGGAAGTAGGATTATTTTGACAACTCGAGAAAAAGGAAGTGGCTTTGCATGGAAAAAGCTG	2004
Rpi-blb2	AAAGGAAGTAGAATTATTTTGACAACTCGAGAAAAAGGAAGTGGCTTTGCATGGAAAAAGCTC	2034
	*****	*****
Mi1.1	AACACTGATCCTCTTTGACCTTCGATTGCTAAGACCAGATGAAAGTTGGGAACATTATAGAG	2061
Mi1.2	AACACTGATCCTCTTTGACCTTCGATTGCTAAGACCAGATGAAAGTTGGGAACTTTATAGAT	2064
Rpi-blb2	TACACTGATCCTCTTTAACCTTCGATTGCTAAGATCAGAAAGAAAGTTGGGAGTTATATAGAG	2094
	*****	*****
Mi1.1	AAAAAGGCATTTGGGAATGAGAGTTGCCCTGATGAACATTATAGATGTCGGTAAAGAAAATA	2121
Mi1.2	AAAAAGGACATTTGGTAATGAGAGTTGCCCTGATGAACATTATAGATGTCGGTAAAGAAAATA	2124
Rpi-blb2	AAAAAGGCATTTGGAAACGAGAGTTGCCCTGATGAACATTATAGATGTTGGTAAAGAAAATA	2154
	*****	*****
Mi1.1	GCCGAAAAATTGTAAAGGGCTTCCTTTGGTGGCTGATCTGATTCGCTGGAGTCATTGCTGGG	2181
Mi1.2	GCCGAAAAATTGTAAAGGGCTTCCTTTGGTGGCTGATCTGATTCGCTGGAGTCATTGCTGGG	2184
Rpi-blb2	GCCGAAAAATTGTAAAGGGCTTCCTTTGGTGGTGGATCTGATTCGCTGGAAATCATTCGCTGGG	2214
	*****	*****
Mi1.1	AGGGAAGAAAAAGGAGTGTGTGGCTTGAAGTTCAAAGTAGTTTGAGTTCTTTTATTTTG	2241
Mi1.2	AGGGAAGAAAAAGGAGTGTGTGGCTTGAAGTTCAAAGTAGTTTGAGTTCTTTTATTTTG	2244
Rpi-blb2	AGGGAAGAAAAAGAGTGTGTGGCTTGAAGTTGTAATAAATTTGCATTCCTTTATTTTG	2274
	*****	*****

Figure 16 (cont.)

Mi1.1	AACAGTGAAGTGAAGTGATGAAGTTATAGAAATTAAGTTATGACCATTACCACATCAC	2301
Mi1.2	AACAGTGAAGTGAAGTGATGAAGTTATAGAAATTAAGTTATGACCATTACCACATCAC	2304
Rpi-blb2	AAGAAATGAAGTGAAGTGATGAAGTTATAGAAATTAAGTTATGACCATTACCAGATCAC	2334
	** * *****	*****
Mi1.1	CTCAAGCCCATGCTTGCCTGATTTTGCAAGTTTCCGAAGGACACTTCATTGACAATCTAT	2361
Mi1.2	CTCAAGCCCATGCTTGCCTGATTTTGCAAGTTTGGCCGAAGGACACTCTTTTGACAATCTAT	2364
Rpi-blb2	CTGAAGCCCATGCTTGCCTGATTTTGCAAGTTGCGCCGAAGGACTGGGTAAACGACAATCCAT	2394
	** *****	*****
	GAGTTGAATGTTTATTTTCGGTGCCTGAAGGATTTGTGGGAAAGACGGAGATGAACAGTATG	2421
Mi1.2	TTGTTTACTGTTTATTTTGGGTGCTGAAGGATTTGTGGGAAAGACGGAGATGAAGGGTATA	2424
Rpi-blb2	GAGTTGAAACCTTATTTGGGGTTTGAAGGATTTGTGGGAAAGACAGATATGAAGAGTCTG	2454
	*** * ** **	*****
	GAAGAAGTGGTGAAGATTTTATATGGATGATTTAATTTACAGTAGCTTGGTAATTTGTTTC	2481
Mi1.2	GAAGAAGTGGTGAAGATTTTATATGGATGATTTAATTTCCAGTAGCTTGGTAATTTGTTTC	2484
Rpi-blb2	GAAGAAGTGGTGAAGATTTTATTTGGATGATTTAATTTCCAGTAGCTTGGTAATTTGTTTC	2514
	*****	*****
	AATGAGATAGGTTATGCACCTGAATTTCCAAATTCATGATCTTGTGCATGACTTTTGTTC	2541
Mi1.2	AATGAGATAGGTTATGATATACCTGAATTTCCAAATTCATGATCTTGTGCATGACTTTTGTTC	2544
Rpi-blb2	AATGAGATAGGTTATGATACCTGACTTGCCTGATCTTGTGCATGACTTTTGTTC	2574
	*****	*****
	ATAAAGCAAGAAAGGAAAAATTTGTTGATCAGATAAGATCAAGTGCTCCATCAGATTG	2601
Mi1.2	ATAAAGCAAGAAAGGAAAAATTTGTTGATCGGATAAGATCAAGTGCTCCATCAGATTG	2604
Rpi-blb2	ATAAAGCAAGAAAGGAAAAATTTGTTGATCGGATAAGATCAAGTGCTCCATCAGATTG	2634
	*****	*****
	TTGCCCTCGTCAAAATTACCATTGATTTGTGATGAGGAGGAG---	2658

Figure 16 (cont.)

Mi1.2	TTGCCCTCGTCAAAATTACCATTTGATTATGATGAGGAGGAGCACTTTGGGCTTAATTTT	2664
Rpi-blb2	TTGCCACGTCAAAATTAGCATTTGATTATGATGATGATGAAGAGCACTTTGGGCTTAATTTT	2694
	*****	*****
Mi1.1	GTCAATGTTTCGATTCAAATAAGAAAAGGCATTTCTGGTAAACACCTCTATTCTTTGAGGATA	2718
Mi1.2	GTCAATGTTTCGATTCAAATAAGAAAAGGCATTTCTGGTAAACACCTCTATTCTTTGAGGATA	2724
Rpi-blb2	GTCCCTGTTTCGGTTCAAATAAGAAAAGGCATTTCCGGTAAACACCTCTATTCTTTGAGCCATA	2754
	*****	*****
Mi1.1	ATTGGAGACCAGCTGGATGACAGTGTTCCTGATGCATTTCCACCTAAGACACTTGAGGCCTT	2778
Mi1.2	AATGGAGACCAGCTGGATGACAGTGTTCCTGATGCATTTCCACCTAAGACACTTGAGGCCTT	2784
Rpi-blb2	AATGGAGATGAGCTGGACGACCATCTTCTTGATACATTTTCATCTAAGACACTTGAGGCCTT	2814
	* *****	*****
Mi1.1	CTTAGAGTGTGGACCTGCATACGTCCTTTTATCATGGTGAAAGATTCTTTGCTGAATGAA	2838
Mi1.2	ATTAGAGTGTGGACCTGGAACCCCTCTTTAAATCATGGTGAAATGATTCCTTTGCTGAATGAA	2844
Rpi-blb2	CTTAGAACCCTTGCACCTGGAATCCTCTTTATCATGGTTAAAGATTCTTTGCTGAATGAA	2874
	*****	*****
Mi1.1	ATATGCATGTTGAATCATTTGAGGTACTTATCCATTGACACACACAAGTTAAATATCTGCCT	2898
Mi1.2	ATATGCATGTTGAATCATTTGAGGTACTTAAAGAATTCGGACACACAAGTTAAATATCTGCCT	2904
Rpi-blb2	ATATGCATGTTGAATCATTTGAGGTACTTAAAGCATTGGACACAGAAGTTAAATCTCTGCCT	2934
	*****	*****
Mi1.1	TTGTCCTTCTCAAACCTCTGGAATCTAGAAAAGCCTGTTTGTGTCCTACCAACAGATCAATC	2958
Mi1.2	TTCTCTTTCTCAAACCTCTGGAATCTAGAAAAGTCTGTTTGTGTCCTAACAAAGGATCAATC	2964
Rpi-blb2	TTGTCCTTCTCAAACCTCTGGAATCTAGAAAATCTTGTTTGTGGATAACAAAAGAATCAACC	2994
	** *****	*****
Mi1.1	TTGGTACTATTACCGAGAATTTTGGATCTTGTAAGTTGCGAGTGTCTCCGTGGATGCT	3018
Mi1.2	TTGGTACTATTACCGAGAATTTTGGATCTTGTAAGTTGCGAGTGTCTCCGTGGGTGCT	3024

Figure 16 (cont.)

Rpi-blb2	TTGATACTATTACCGAGAAATTTGGGATCTTGTAAGTTGCAAGTTGCTGTTCACTGCTGCT 3054 *** ***** * * * *
Mi1.1	TGTTCTTTCTTTGATATGGATGCAGATGAATCAATATTGATAGCAGAGGACACAAAGTTA 3078
Mi1.2	TGTTCTTTCTTTGATATGGATGCAGATGAATCAATATTGATAGCAAGGACACAAAGTTA 3084
Rpi-blb2	TGTTCTTTCTTTGATATGGATGCAGATGAATCAATATTGATAGCAGAGGACACAAAGTTA 3114 ***** * * * *
Mi1.1	GAGAACTTGAGAAATATTAAACGGAACTGTTGATTTCCCTATTTCGAAAGATACAAAGAATATT 3138
Mi1.2	GAGAACTTGAGAAATATTAGGGGAACGTGTTGATTTCCCTATTTCGAAAGATACAAAGAATATT 3144
Rpi-blb2	GAGAACTTGACAGCATTAGGGGAACTCGTGCTTTCCCTATTTCGAAAGATACAGAGGATATT 3174 ***** * * * *
Mi1.1	TTCAAAAGGTTTCCCAATCTTCAGTTGCTTTTCATTTGAACTCAAGGAGTCATGGGATTAT 3198
Mi1.2	TTCAAAAGGTTTCCCAATCTTCAGGTGCTTCAGTTTGAACCTCAAGGAGTCATGGGATTAT 3204
Rpi-blb2	TTCAAAAGGCTTCCCAATCTTCAAGTGCTTCATTTCAAACTCAAGGAGTCATGGGATTAT 3234 ***** * * * *
Mi1.1	TCAACAGAGCAACATTGGTTCTCGGAATTGGATTTCCTTAACCTGAAC TAGAAACACTCTCT 3258
Mi1.2	TCAACAGAGCAACATTGGTTCCCGAAATTGGATTGCCCTAAGTGAAC TAGAAACACTCTGT 3264
Rpi-blb2	TCAACAGAGCAATATTGGTTCCCGAAATTGGATTCCCTAAGTGAAC TAGAAAACTCACT 3294 ***** * * * *
Mi1.1	GTAGGTTTTAAAAGTTCAAACACAAACGATAGTGGGTCCCTCTGTAGCGACAAATCGGCCG 3318
Mi1.2	GTAGGTTTTAAAAGTTCAAACACAAACCACTGTGGGTCCCTCTGTGTGACAAATCGGCCG 3324
Rpi-blb2	GTAGATTTTGAAAGATCAAACACAAATGACAGTGGGTCCCTCTGTGAGCCATAAATCGGCCA 3354 ***** * * * *
Mi1.1	TGGGATTTTCACTTCCCTTCAAATTTGAAAAATACGTGTTGGTTGCGTGAATTTCCGCTGACA 3378
Mi1.2	TGGGATTTTCACTTCCCTTCAAATTTGAAAAAAGTGTGTTGTATGACTTCCCTCTGACA 3384
Rpi-blb2	TGGGATTTTCACTTCCCTTCGAGTTTGAAAAAGATTGCAATTGCATGAATTTCCCTCTGACA 3414

Figure 16 (cont.)

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*****
***** * ***** * * * * * * * * * * * * * * * *
Mi1.1 TCCGATTCACTATCAACAATAGCGAGACTGCCCAACCTTGAAGAGTTGTCCCTTTATCAT 3438
Mi1.2 TCCGATTCACTATCAACAATAGCGAGACTGCCCAACCTTGAAGAGTTGTCCCTTTATGAT 3444
Rpi-blb2 TCCGATTCACTATCAACAATAGCGAGACTGCTGAACCTTGAAGAGTTGACCTTTATCGT 3474
*****
***** * * * * * * * * * * * * * * * *
Mi1.1 ACAATCATCCATGGAGAAGAAATGGAACATGGGGGAGGAAGACACCTTTGAGAAATCTCAAA 3498
Mi1.2 ACAATCATCCAGGGAGAAGAAATGGAACATGGGGGAGGAAGACACCTTTGAGAAATCTCAAA 3504
Rpi-blb2 ACAATCATCCATGGGAAGAAATGGAACATGGGAGAAGAACACACCTTTGAGAAATCTCAAA 3534
*****
***** * * * * * * * * * * * * * * * *
Mi1.1 TTTTGAACCTTCAATCAAGTTAGTATTTTCCAAGTGGGAGGTGGAGAGGAATCCTTCCCC 3558
Mi1.2 TTTTGAACCTTGGCTACTGACTCTTTCCAAGTGGGAGGTGGAGAGGAATCCTTCCCC 3564
Rpi-blb2 TGTGTGATGTTGAGTCAAGTGATTCCTTCCAAGTGGGAGGTGGAGAGGAATCCTTCCCC 3594
*****
***** * * * * * * * * * * * * * * * *
Mi1.1 AATCTTGAGAAATTAAGAACTGCGGGATGTCATAAGCTAGAGGAGATTCACCTAGTTTT 3618
Mi1.2 AATCTTGAGAAATTAAGAACTGAGGAATGTGGTAAGCTTGAGGAGATTCACCTAGTTTT 3624
Rpi-blb2 ACGTTGAGAAATTAGAACTGTCGACTGTCATAATCTTGAGGAGATTCGCTAGTTTT 3654
*****
***** * * * * * * * * * * * * * * * *
Mi1.1 GGAGATATTTATTCATTGAAATCTATCAAAAATGTAAAGAGTCCTCAACTGAAGATTC 3678
Mi1.2 GGAGATATTTATTCATTGAAATTTATCAAAAATGTAAAGAGTCCTCAACTGAAGATTC 3684
Rpi-blb2 GGGATATTTATTCCTTGAAATTTATCGAACTTGTAAGGAGCCCTCAACTGAAAATCC 3714
*****
***** * * * * * * * * * * * * * * * *
Mi1.1 GCTCTCAAAATTAAGGAATACGCTGAAGATATGAGGGAGGGACGAGCTTCAGATCCTT 3738
Mi1.2 GCTCTCAAGATTAAGAAATACGCTGAAGATATGAGAGGAGGGAACGATCTCAGATCCTT 3744
Rpi-blb2 GCTCTCAAGATTAAGGAATATGCTGAAGATATGAGGGAGGGGACGAGCTTCAGATCCTT 3774
*****
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Figure 16 (cont.)

Mi1.1	GGCCAAAAGAATATCCCCTTATTTAAGTAG	3768
Mi1.2	GGCCAGAAGAATATCCCCTTATTTAAGTAG	3774
Rpi-blb2	GGCCAGAAGGATATCCCCTTATTTAAGTAG	3804

Figure 17: Multiple Sequence Alignments of Mil.1.1, Mil.1.2 and Rpi-blb2 proteins

```
CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: Mil.1      1255 aa
Sequence 2: Mil.1.2    1257 aa
Sequence 3: Rpi-blb2    1267 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 91
Sequences (1:3) Aligned. Score: 82
Sequences (2:3) Aligned. Score: 81
Guide tree file created: [ /ebi/externserv/clustalw-work/interactive/clustalw-20040503-14322840.dnd]
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1: Sequences: 2      Score:25939
Group 2: Sequences: 3      Score:24668
Alignment Score 19405
CLUSTAL-Alignment file created [ /ebi/externserv/clustalw-work/interactive/clustalw-20040503-14322840.aln]

CLUSTAL W (1.82) multiple sequence alignment

Mi1.1      MEKRDNEEANNLSVLFSALSKDIADVIVFLE---NEENQKALDKDQVEKIKLKMAFICT 57
```

Figure 17 (cont.)

Mi 1.2	MEKRKIDEEANNLSVFSALSKDIANVLI FLE---NEENQKALDKDQVEKIKLKMAFICT	57
Rpi-blb2	MEKRKIDNEEANNLSVFSALRKDAANVLD FLERLKNEEDQKAVDVDLIESLKLKLT FICT	60

Mi 1.1	YVQLSCSDFEQFEDIMTRKRQEVENLLQPLLLDDD-----VFTSLTSNMDDCISLYHR	109
Mi 1.2	YVQLSYSDFEQFEDIMTRNRQEVENLLQSLLLDDD-----VLTSLTSNMDDCISLYHR	109
Rpi-blb2	YVQLSYSDLKFKFEDIMTRKRQEVENLLQPIILDDDGKDVGCKYVLTSLAGNMDDCISLYHR	120

Mi 1.1	SYKSDAIMMDEQLDFLLNLNLYHLSKHHAEKIFPGVTQYEVVLQNICGNIRD F HGLIVNGCI	169
Mi 1.2	SYKSDAIMMDEQLDFLLNLNLYHLSKHHAEKIFPGVTQYEVVLQNVCGNIRD F HGLILNGCI	169
Rpi-blb2	S-KSDATMMDEQLGFLLLNLNLSHLSKHRAEKMFPGVTQYEVVLQNVCGNIRD F HGLIVNCCI	179

Mi 1.1	KHEMVENVLPFLQLMADRVGHFLWDDQTDEDSRLSELDEDEQNDRDSRLFKIAHLLLKIV	229
Mi 1.2	KHEMVENVLPFLQLMARVGHFLWEDQTDEDSRLSELDEDEHNDRDSRLFQ LTHLLLKIV	229
Rpi-blb2	KHEMVENVLSLFQLMARVGRFLWEDQADEDSQLSELDEDDQNDKDPQLFKIAHLLLKIV	239

Mi 1.1	PVELEVIHCYTNLKASTSAEVLGFIKQLLETSPDILREYLIPLQEHMTVITPSTSGAR	289
Mi 1.2	PTELEVMIHCYTNLKASTSAEVLGRFIKKLLETSPDILREYIIQLQEHMLTVIPSTLGAR	289
Rpi-blb2	PTELEVMIHCYKTLKASTSTEIGRFIKKLLETSPDILREYLIHLQEHMTVITPNTSGAR	299

Mi 1.1	NIHVMMEFLLIILSDMP-KDFIHHDKLFDLLDRVGVLTREVSTLV RDLEEEPRNKEGNNQ	348
Mi 1.2	NIHVMMEFLLIILSDMP-KDFIHHDKLFDLLAHVGTLTREVSTLV RDLEEKLRNKEGNNQ	348
Rpi-blb2	NIHVMMEFLLIILSDMPPKDFIHHDKLFDLLARVVALTREVSTLV RDLEEKLRKESTDE	359

Mi 1.1	TNCATLDLLENIELKKDLKHVYLKALDSSQCCFPMSDGP LFMHLLIHIHNDLDSNAYS	408
Mi 1.2	TNCATLDLLENIELKKDLKHVYLKAPNSQCCFPMSDGP LFMHLLHMHNLNDLDSNAYS	408

Figure 17 (cont.)

Rpi-blb2	TNCATLKFLLENIELLKEDLKHVYLKVPDSSQYCFPMSDGPLFMHLLQRLHLLDLDLDSNAYS 419 *****.:*****:*****.:*** *****:***:*****
Mi1.1	IALIKEIEIELVKQDLKFIIRFFVD-AEQGLYKDLWARVLDVAYEAKDVIDSIIVRDNGLL 467
Mi1.2	ISLIEIEIELVSQELEFIIRFFGDAAEQGLYKDIWARVLDVAYEAKDVIDSIIVRDNGLL 468
Rpi-blb2	IALIKEQIGLVKEDLEFIIRFFAN-IEQGLYKDLWERVLDVAYEAKDVIDSIIVRDNGLL 478 *.:*****.:***:*****.:*****:*** *****:***:*****
Mi1.1	HLIFSLPITIKIKLIKKEEISALDENI PKDRGLIVNSPKKPVERKSITTDKIITVGFEEE 527
Mi1.2	HLIFSLPITIKIKLIKKEEISALDENI PKDRGLIVNSPKKPVERKSITTDKIIVGFEEE 528
Rpi-blb2	HLIFSLPITIRKKNMLIKEEVSDLHENI SKNRGLIVNSPKKPVERKSITTDKIIVGFEEE 538 ***** **.:*****:*.***.:*****:***** ***** ** **
Mi1.1	TNLI LRKLTSGSADLDVISITGMPGSGKTTLAYKVYNDKSVSRFDLRAWCTVDQGCDEK 587
Mi1.2	TNLI LRKLTSGPADLDVISITGMPGSGKTTLAYKVYNDKSVSRHFDLRAWCTVDQGYDDK 588
Rpi-blb2	TNLI LRKLTSGPADLDVISIIGMPGLGKTTLAYKVYNDKSVSHFDLRAWCTVDQVYDEK 598 *****.:***** ***** *****:***** *.:*
Mi1.1	KLNTIFSQVSDSKLSENIDVADKLKQKQKRYLIVLDDVDWDTTWDDELTRPFPEK 647
Mi1.2	KLDTIFSQVSGSDSNISENIDVADKLKQKQKRYLIVLDDVDWDTTLDDELTRPFPEAK 648
Rpi-blb2	KLDDKIFNQVSDSNSKLSENIDVADKLKQKQKRYLIVLDDVDWDTNTWDDELTRPFPDGM 658 ***:*.***.*.:*****:*****:*****.* *****:.
Mi1.1	KGSRIILTTRKEVALHGKINTDPLDLRLRPDESWELEKRAFNESCPDELLDVGKEI 707
Mi1.2	KGSRIILTTRKEVALHGKINTDPLDLRLRPDESWELEKRTFGNESCPDELLDVGKEI 708
Rpi-blb2	KGSRIILTTRKEKKVALHGKLYTDPLNLRLLRSEESWELEKRAFNESCPDELLDVGKEI 718 *****:***** *****:*****.:*****:*****:*****
Mi1.1	AENCKGLPLVADLLIAGVIAGREKKRSVWLEVQSSLSFIINSEVEVMKVIELSYDHLPHH 767
Mi1.2	AENCKGLPLVADLLIAGVIAGREKKRSVWLEVQSSLSFIINSEVEVMKVIELSYDHLPHH 768
Rpi-blb2	AENCKGLPLVVDLLIAGIAGREKKRSVWLEVVNNLHSFILKNEVEVMKVIEISYDHLPDH 778

Figure 17 (cont.)

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*****.*****:*****:*****..* *****:*****:*****.*
Mi 1.1 LKPCLLYFASFEPKDTSLTIYELNVYFGAEGFVGKTEMNSMEVVVKIYMDDLIYSSLVICF 827
Mi 1.2 LKPCLLHFASWPKDTPTIYLFYLGAEFGEKTEMKGIEEVVKIYMDDLISSLVICF 828
Rpi-blb2 LKPCLLYFASAPKDWTTIHCLKIWGFEGVEKTMKSLEEVVKIYLDLSSLVICF 838
*****:*** ***: **: * *****:**** *****
Mi 1.1 NEIGYALNFQIHDLVHDFCLIKARKENLFDQIRSSAPSDLLPRQITIDCDEEE-HFGINF 886
Mi 1.2 NEIGDIILNFQIHDLVHDFCLIKARKENLFDRISSAPSDLLPRQITIDYDEEEHFGINF 888
Rpi-blb2 NEIGDYPTCQLHDLVHDFCLIKARKEKLCDRISAPSDLLPRQISIDYDDDEEHFGINF 898
**** .*:*****:*****:*** *****:*** *:*****
Mi 1.1 VMFDSNKKRHSGKHLYSRLRIGDQLDDSVSDAFHLRHLRLRLVLDLHSTFIMVKDSLNE 946
Mi 1.2 VMFDSNKKRHSGKHLYSRLRIGDQLDDSVSDAFHLRHLRLRLVLDLEPSLIMVNDLNE 948
Rpi-blb2 VLFSGNKKRHSGKHLYSRLTINGDELDDHLSDTFHLRHLRLRLTHLESSFIMVKDSLNE 958
*.*.*****:***** * ***:*** **:*****:*. *.*.***:*****
Mi 1.1 ICMLNHLRYLSIDTQVKYLPFSFNLWNLESFVSTNRSILVLLPRILDLVKLRVLSVDA 1006
Mi 1.2 ICMLNHLRYLRITQVKYLPFSFNLWNLESFVSNKGSILVLLPRILDLVKLRVLSVGA 1008
Rpi-blb2 ICMLNHLRYLSIGTEVKSLPLFSFNLWNLEILFVDNKESTLILPRIWDLVKLQVLTFTA 1018
***** * *.* ***:***** ***.: * *.* *****:*** . *
Mi 1.1 CSFFDMDADESILIAEDTKLENLRILTELLISYSKDTKNIFKRFPNLQLLSFELKESWDY 1066
Mi 1.2 CSFFDMDADESILIAKDTKENLRILGELLISYSKDTMNIKRFPNLQVLQFELKESWDY 1068
Rpi-blb2 CSFFDMDADESILIAEDTKLENLTALGEIVLSYWKDTEIDFKRLPNLQVLHFKLKESWDY 1078
*****:***** * ***:*** ***:***:*****:***:*****
Mi 1.1 STEQHWFSELDLFTLETLVSGFKSSNTNDSGSSVATNRPWDFHFPNKLKILWLREFPLT 1126
Mi 1.2 STEQHWFPKLDLFTLETLVCGFKSSNTNHCSSVVTNRPWDFHFPNKLKELLYDFPLT 1128
Rpi-blb2 STEQYWFPKLDLFTLEKLTVDERSNTNDSGSSAAINRPWDFHFPSSIKRIQLHEFFPLT 1138
*****:*** ***:*** *.*: *****.****.*****:*** * *.*:****
```

Figure 17 (cont.)

Mi 1.1	SDSLSTIARLPNLEELSLYHTIIHGEEWNMGEEDTFENLKFLNFQVSI SKWEVGEESFP	1186
Mi 1.2	SDSLSTIARLPNLEENLSYDTIIQGEENMGEEDTFENLKFLNRLTLT SKWEVGEESFP	1188
Rpi-blb2	SDSLSTIARLNLLEELLYRTIIHGEEWNMGEEDTFENLKCLMLSQVILSKWEVGEESFP	1198
	***** * * * * : *****	
Mi 1.1	NLEKLRGCHKLEETPPSFGDIYSLKSIKIVKSPQLEDSALKIKIKEYAEDMRGGDELQIL	1246
Mi 1.2	NLEKLRQECGKLEETPPSFGDIYSLKFIKIVKSPQLEDSALKIKIKEYAEDMRGGNDLQIL	1248
Rpi-blb2	TLEKLELSDCHNLEETPPSFGDIYSLKIEIVRSPQLENSALKIKIKEYAEDMRGGDELQIL	1258
	. ***** * * : ***** : *****	
Mi 1.1	GQKNIPLEK	1255
Mi 1.2	GQKNIPLEK	1257
Rpi-blb2	GQKDIPLEK	1267
	*** : *****	

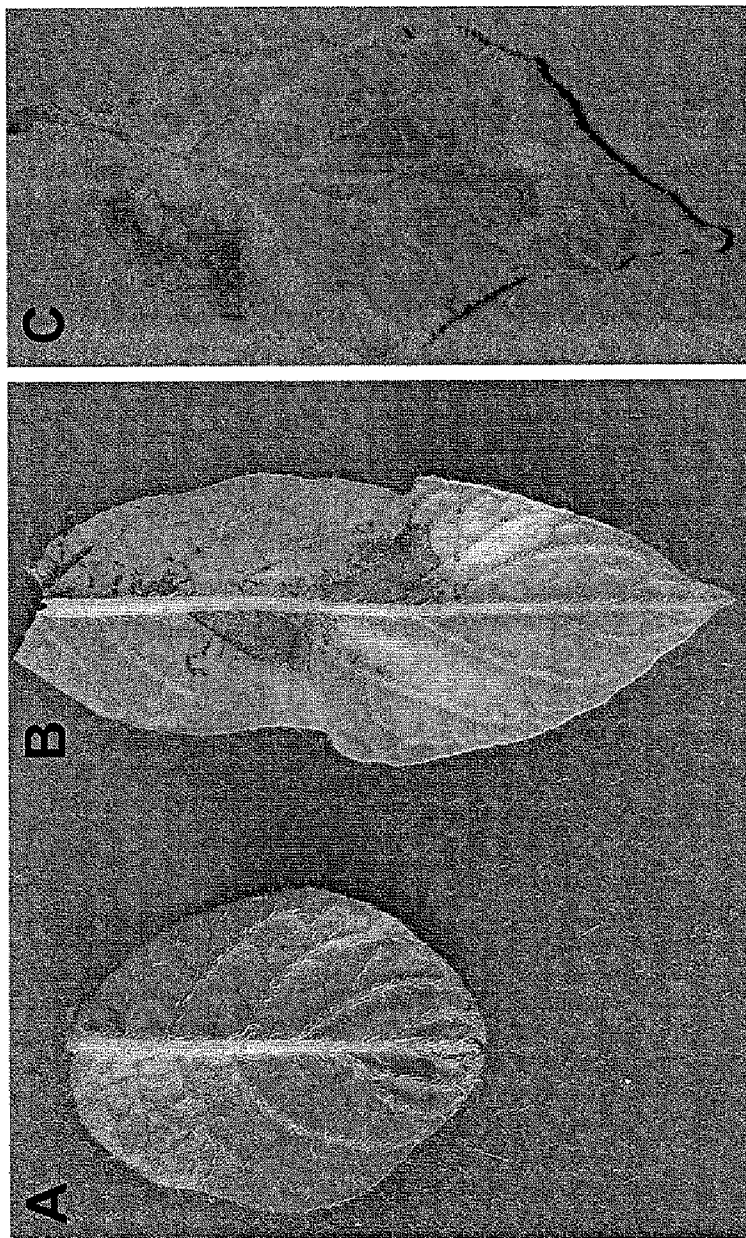


Figure 18